10-088-417

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 14:45:41 ; Search time 122 Seconds
(without alignments)
88.765 Million cell updates/sec

Title: US-10-088-417A-1
Perfect score: 132
Sequence: 1 KIAALKQKIASLKQEIDALEYENDALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 794064

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	132	100.0	28	4	AAB74343	Aab74343 Peptide S
2	132	100.0	28	4	AAB74351	Aab74351 Peptide S
3	132	100.0	28	8	ADM41436	Adm41436 Self-asse
4	129	97.7	28	4	AAB74341	Aab74341 Peptide S
5	129	97.7	28	4	AAB74342	Aab74342 Peptide S
6	85	64.4	28	8	ADM41438	Adm41438 Self-asse
7	82	62.1	28	4	AAB74345	Aab74345 Peptide S
8	80	60.6	27	8	ADM41437	Adm41437 Self-asse
9	76	57.6	28	4	AAB74348	Aab74348 Peptide S
10	76	57.6	28	4	AAB74356	Aab74356 Peptide u
11	76	57.6	28	4	AAB74352	Aab74352 Peptide S
12	75	56.8	28	4	AAB74346	Aab74346 Peptide S
13	75	56.8	28	4	AAB74347	Aab74347 Peptide S
14	74	56.1	28	4	AAB74349	Aab74349 Peptide S
15	70	53.0	28	4	AAB74355	Aab74355 Peptide u
16	70	53.0	28	4	AAB74350	Aab74350 Peptide S
17	57	43.2	28	7	ABR84737	Abr84737 DE novo d
18	54	40.9	28	7	ABR84736	Abr84736 DE novo d
19	52	39.4	17	4	AAB74344	Aab74344 Peptide C
20	52	39.4	24	5	AAE18799	Aae18799 Strep pep
21	52	39.4	24	5	AAE18797	Aae18797 Strep pep
22	52	39.4	25	3	AAY95958	Aay95958 Coiled-co
23	52	39.4	25	3	AAB08381	Aab08381 Peptide u
24	52	39.4	25	3	AAB08382	Aab08382 Peptide u
25	52	39.4	27	5	AAE18788	Aae18788 CVX0270 p
26	51	38.6	28	4	AAB50879	Aab50879 Integrin
27	51	38.6	28	4	AAB59138	Aab59138 Alpha-hel
28	50	37.9	23	3	AAB08388	Aab08388 Peptide u
29	50	37.9	23	6	ADA00699	Ada00699 Protein m
30	46	34.8	18	4	AAB74340	Aab74340 Peptide C
31	46	34.8	24	2	AAW11601	Aaw11601 Lactam br
32	46	34.8	24	3	AAB21683	Aab21683 Colied co
33	46	34.8	24	7	ADD93917	Add93917 Coiled co
34	46	34.8	28	2	AAR31979	Aar31979 SSP4 poly
35	45	34.1	24	2	AAW11604	Aaw11604 Generic l
36	45	34.1	28	7	ABR84735	Abr84735 DE novo d
37	44	33.3	14	2	AAW71415	Aaw71415 Peptide f
38	44	33.3	15	2	AAW71416	Aaw71416 Peptide f
39	44	33.3	15	2	AAW80531	Aaw80531 Beta-shee
40	44	33.3	16	2	AAW80546	Aaw80546 Peptide h
41	44	33.3	18	2	AAW71424	Aaw71424 Peptide h
42	44	33.3	21	4	AAG65530	Aag65530 Antimicro
43	44	33.3	24	3	AAB21684	Aab21684 Colied co
44	44	33.3	24	7	ADD93918	Add93918 Coiled co
45	41	31.1	21	5	ABG78944	Abg78944 Human bre

ALIGNMENTS

RESULT 1
AAB74343
ID AAB74343 standard; peptide; 28 AA.
XX
AC AAB74343;
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p1C.
XX
KW Atomic Force Microscopy; AFM.
XX
OS Unidentified.
XX
PN WO200121646-A1.
XX
PD 29-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-GB003576.
XX
PR 17-SEP-1999; 99GB-00022013.
XX
PA (UYSU-) UNIV SUSSEX.
XX
PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX
DR WPI; 2001-335468/35.
XX
PT New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
PS Claim 16; Page 26; 45pp; English.
XX
CC The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p1C
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 132; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDALEYENDALEQ 28
||||||||||||||||||||||||||||

```
Db          1 KIAALKQKIASLKQEIDALEYENDALEQ 28

RESULT 2
AAB74351
ID   AAB74351 standard; peptide; 28 AA.
XX
AC   AAB74351;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p1.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Claim 16; Page 26; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is the peptide monomer unit SAF-p1
XX
SQ   Sequence 28 AA;

  Query Match             100.0%;  Score 132;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-11;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALEYENDALEQ 28
              ||||||||||||||||||||||||||||
Db          1 KIAALKQKIASLKQEIDALEYENDALEQ 28


RESULT 3
ADM41436
ID   ADM41436 standard; peptide; 28 AA.
XX
AC   ADM41436;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Self-assembling peptide fibre SAF-p1.
XX
KW   Fibre-shaping peptide; self-assembling peptide.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal NH3 moiety"
XX
PN   WO2004022584-A1.
XX
PD   18-MAR-2004.
XX
PF   08-SEP-2003; 2003WO-GB003900.
XX
PR   06-SEP-2002; 2002GB-00020805.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson D,  Ryadnov MG;
XX
DR   WPI; 2004-248444/23.
XX
PT   Novel fiber-shaping peptide comprising hub and several peptide monomer
PT   units, useful for producing protein structure useful in purification of
PT   biological fluids and in surface engineering procedures.
XX
PS   Example 30; Page 22; 37pp; English.
XX
CC   The present sequence is that of self-assembling peptide fibre (SAF) SAF-
CC   p1. The invention relates to fibre-shaping (FiSh) peptides ADM41434-
CC   ADM41435 that are capable of interacting with SAFs to form protein
CC   structures. The FiSh peptides allow morphological changes (branches,
CC   splits, kinks and bends) to be made to protein fibres comprising SAFs. By
CC   incorporating such morphological changes in the protein fibres, it is
CC   possible to generate a variety of (nanoscale) protein structures, such as
CC   assemblies in general, including matrix, filter, network, grid and
CC   scaffold structures. Use of the protein structures in the purification of
CC   biological fluids, for assembling cells for cell and tissue engineering,
CC   and in surface engineering procedures is claimed.
XX
SQ   Sequence 28 AA;

  Query Match             100.0%;  Score 132;  DB 8;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-11;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALEYENDALEQ 28
              ||||||||||||||||||||||||||||
Db          1 KIAALKQKIASLKQEIDALEYENDALEQ 28


RESULT 4
AAB74341
ID   AAB74341 standard; peptide; 28 AA.
XX
AC   AAB74341;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p1A.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
```

```
XX
PS   Claim 16; Page 26; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is the peptide monomer unit SAF-p1A
XX
SQ   Sequence 28 AA;

  Query Match             97.7%;  Score 129;  DB 4;  Length 28;
  Best Local Similarity   96.4%;  Pred. No. 7e-11;
  Matches   27;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALEYENDALEQ 28
              ||||||||||:||||||||||||||||||
Db          1 KIAALKQKIAALKQEIDALEYENDALEQ 28


RESULT 5
AAB74342
ID   AAB74342 standard; peptide; 28 AA.
XX
AC   AAB74342;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p1B.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Disclosure; Page 9; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is the peptide monomer unit SAF-p1B
XX
SQ   Sequence 28 AA;

  Query Match             97.7%;  Score 129;  DB 4;  Length 28;
  Best Local Similarity   96.4%;  Pred. No. 7e-11;
  Matches   27;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALEYENDALEQ 28
              ||||||||||:||||||||||||||||||
Db          1 KIAALKQKIAALKQEIDALEYENDALEQ 28


RESULT 6
ADM41438
ID   ADM41438 standard; peptide; 28 AA.
XX
AC   ADM41438;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Self-assembling peptide fibre SAF-p2a.
XX
KW   Fibre-shaping peptide; self-assembling peptide.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal NH3 moiety"
XX
PN   WO2004022584-A1.
XX
PD   18-MAR-2004.
XX
PF   08-SEP-2003; 2003WO-GB003900.
XX
PR   06-SEP-2002; 2002GB-00020805.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson D,  Ryadnov MG;
XX
DR   WPI; 2004-248444/23.
XX
PT   Novel fiber-shaping peptide comprising hub and several peptide monomer
PT   units, useful for producing protein structure useful in purification of
PT   biological fluids and in surface engineering procedures.
XX
PS   Example 36; Page 22; 37pp; English.
XX
CC   The present sequence is that of self-assembling peptide fibre (SAF) SAF-
CC   p2a. The invention relates to fibre-shaping (FiSh) peptides ADM41434-
CC   ADM41435 that are capable of interacting with SAFs to form protein
CC   structures. The FiSh peptides allow morphological changes (branches,
CC   splits, kinks and bends) to be made to protein fibres comprising SAFs. By
CC   incorporating such morphological changes in the protein fibres, it is
CC   possible to generate a variety of (nanoscale) protein structures, such as
CC   assemblies in general, including matrix, filter, network, grid and
CC   scaffold structures. Use of the protein structures in the purification of
CC   biological fluids, for assembling cells for cell and tissue engineering,
CC   and in surface engineering procedures is claimed.
XX
SQ   Sequence 28 AA;

  Query Match             64.4%;  Score 85;  DB 8;  Length 28;
  Best Local Similarity   75.0%;  Pred. No. 9.5e-05;
  Matches   21;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALEYENDALEQ 28
              ||  |||| | ||||| |||||  ||||
Db          1 KIRRLKQKNARLKQEIAALEYEIAALEQ 28


RESULT 7
AAB74345
ID   AAB74345 standard; peptide; 28 AA.
XX
AC   AAB74345;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p2A.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
```

PN WO200121646-A1.
XX
PD 29-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-GB003576.
XX
PR 17-SEP-1999; 99GB-00022013.
XX
PA (UYSU-) UNIV SUSSEX.
XX
PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX
DR WPI; 2001-335468/35.
XX
PT New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
PS Disclosure; Page 9; 45pp; English.
XX
CC The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p2A
XX
SQ Sequence 28 AA;

Query Match 62.1%; Score 82; DB 4; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.00025;
Matches 21; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDALEYENDALEQ 28
||:||| | ||||||| ||| | ||||
Db 1 KISALKWKNASLKQEIAALEQEIAALEQ 28

RESULT 8
ADM41437
ID ADM41437 standard; peptide; 27 AA.
XX
AC ADM41437;
XX
DT 03-JUN-2004 (first entry)
XX
DE Self-assembling peptide fibre (SAF).
XX
KW Fibre-shaping peptide; self-assembling peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal NH3 moiety"
XX
PN WO2004022584-A1.
XX
PD 18-MAR-2004.
XX
PF 08-SEP-2003; 2003WO-GB003900.
XX
PR 06-SEP-2002; 2002GB-00020805.
XX
PA (UYSU-) UNIV SUSSEX.
XX
PI Woolfson D, Ryadnov MG;
XX
DR WPI; 2004-248444/23.
XX
PT Novel fiber-shaping peptide comprising hub and several peptide monomer
PT units, useful for producing protein structure useful in purification of
PT biological fluids and in surface engineering procedures.
XX
PS Example 30; Page 22; 37pp; English.
XX
CC The present sequence is that of a self-assembling peptide fibre (SAF).
CC The invention relates to fibre-shaping (FiSh) peptides ADM41434-ADM41435
CC that are capable of interacting with SAFs to form protein structures. The
CC FiSh peptides allow morphological changes (branches, splits, kinks and
CC bends) to be made to protein fibres comprising SAFs. By incorporating
CC such morphological changes in the protein fibres, it is possible to
CC generate a variety of (nanoscale) protein structures, such as assemblies
CC in general, including matrix, filter, network, grid and scaffold
CC structures. Use of the protein structures in the purification of
CC biological fluids, for assembling cells for cell and tissue engineering,
CC and in surface engineering procedures is claimed.
XX
SQ Sequence 27 AA;

Query Match 60.6%; Score 80; DB 8; Length 27;
Best Local Similarity 74.1%; Pred. No. 0.00045;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 IAALKQKIASLKQEIDALEYENDALEQ 28
| |||| | ||||| ||||| ||||
Db 1 IRRLKQKNARLKQEIAALEYEIAALEQ 27

RESULT 9
AAB74348
ID AAB74348 standard; peptide; 28 AA.
XX
AC AAB74348;
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p2D.
XX
KW Atomic Force Microscopy; AFM.
XX
OS Unidentified.
XX
PN WO200121646-A1.
XX
PD 29-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-GB003576.
XX
PR 17-SEP-1999; 99GB-00022013.
XX
PA (UYSU-) UNIV SUSSEX.
XX
PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX
DR WPI; 2001-335468/35.
XX
PT New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
PS Disclosure; Page 9; 45pp; English.
XX
CC The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p2D
XX
SQ Sequence 28 AA;

Query Match 57.6%; Score 76; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.0017;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDALEYENDALEQ 28
|| ||| | | ||||| ||| | ||||

```
Db          1 KIRALKAKNAHLKQEIAALEQEIAALEQ 28


RESULT 10
AAB74356
ID   AAB74356 standard; peptide; 28 AA.
XX
AC   AAB74356;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide used to form blunt-ended heterodimers.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Disclosure; Fig 8; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is a peptide used to form blunt-ended heterodimers
XX
SQ   Sequence 28 AA;

  Query Match             57.6%;  Score 76;  DB 4;  Length 28;
  Best Local Similarity   71.4%;  Pred. No. 0.0017;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALEYENDALEQ 28
              || ||| | | ||||| ||| |  ||||
Db          1 KIRALKAKNAHLKQEIAALEQEIAALEQ 28


RESULT 11
AAB74352
ID   AAB74352 standard; peptide; 28 AA.
XX
AC   AAB74352;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p2.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Claim 16; Page 26; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is the peptide monomer unit SAF-p2
XX
SQ   Sequence 28 AA;

  Query Match             57.6%;  Score 76;  DB 4;  Length 28;
  Best Local Similarity   71.4%;  Pred. No. 0.0017;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALEYENDALEQ 28
              || ||| | | ||||| ||| |  ||||
Db          1 KIRALKAKNAHLKQEIAALEQEIAALEQ 28


RESULT 12
AAB74346
ID   AAB74346 standard; peptide; 28 AA.
XX
AC   AAB74346;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p2B.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Disclosure; Page 9; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is the peptide monomer unit SAF-p2B
XX
SQ   Sequence 28 AA;
```

```
  Query Match             56.8%;  Score 75;  DB 4;  Length 28;
  Best Local Similarity   71.4%;  Pred. No. 0.0024;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALEYENDALEQ 28
              || ||| | | ||||| ||| |  ||||
Db          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28


RESULT 13
AAB74347
ID   AAB74347 standard; peptide; 28 AA.
XX
AC   AAB74347;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p2C.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Claim 16; Page 26; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is the peptide monomer unit SAF-p2C
XX
SQ   Sequence 28 AA;

  Query Match             56.8%;  Score 75;  DB 4;  Length 28;
  Best Local Similarity   71.4%;  Pred. No. 0.0024;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALEYENDALEQ 28
              || ||| | | ||||| ||| |  ||||
Db          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28


RESULT 14
AAB74349
ID   AAB74349 standard; peptide; 28 AA.
XX
AC   AAB74349;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p2E.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Disclosure; Page 9; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is the peptide monomer unit SAF-p2E
XX
SQ   Sequence 28 AA;

  Query Match             56.1%;  Score 74;  DB 4;  Length 28;
  Best Local Similarity   71.4%;  Pred. No. 0.0033;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALEYENDALEQ 28
              || ||| | | ||||| ||| |  ||||
Db          1 KIRALKCKNAHLKQEIAALEQEIAALEQ 28


RESULT 15
AAB74355
ID   AAB74355 standard; peptide; 28 AA.
XX
AC   AAB74355;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide used to form blunt-ended heterodimers.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Disclosure; Fig 8; 45pp; English.
XX
```

CC The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is a peptide used to form blunt-ended heterodimers
XX
SQ Sequence 28 AA;

Query Match 53.0%; Score 70; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         15 EIDALEYENDALEQ 28
              ||||||||||||||
Db          1 EIDALEYENDALEQ 14
```

Search completed: April 27, 2005, 15:02:15
Job time : 124 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2005, 15:02:43 ; Search time 89.5 Seconds
(without alignments)
104.113 Million cell updates/sec

Title: US-10-088-417A-1
Perfect score: 132
Sequence: 1 KIAALKQKIASLKQEIDALEYENDALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 334731

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	43.2	28	14	US-10-360-053-23	Sequence 23, Appl
2	54	40.9	28	14	US-10-360-053-22	Sequence 22, Appl
3	52	39.4	27	10	US-09-882-774-7	Sequence 7, Appli
4	51	38.6	28	9	US-09-320-907B-6	Sequence 6, Appli
5	51	38.6	28	15	US-10-447-292-6	Sequence 6, Appli
6	50	37.9	23	10	US-09-259-658-59	Sequence 59, Appl
7	46	34.8	24	14	US-10-338-083-19	Sequence 19, Appl
8	46	34.8	24	16	US-10-611-399-19	Sequence 19, Appl
9	46	34.8	24	17	US-10-794-751-19	Sequence 19, Appl
10	45	34.1	28	14	US-10-360-053-21	Sequence 21, Appl
11	44	33.3	24	14	US-10-338-083-20	Sequence 20, Appl
12	44	33.3	24	16	US-10-611-399-20	Sequence 20, Appl
13	44	33.3	24	17	US-10-794-751-20	Sequence 20, Appl
14	44	33.3	26	16	US-10-630-926-7	Sequence 7, Appli
15	41	31.1	21	9	US-09-834-759-534	Sequence 534, App
16	41	31.1	21	13	US-10-007-805-534	Sequence 534, App
17	41	31.1	21	13	US-10-007-805-587	Sequence 587, App
18	41	31.1	21	14	US-10-076-622-534	Sequence 534, App
19	41	31.1	21	14	US-10-076-622-587	Sequence 587, App
20	41	31.1	21	14	US-10-124-805-534	Sequence 534, App
21	41	31.1	21	14	US-10-124-805-587	Sequence 587, App
22	40	30.3	28	14	US-10-023-066A-70	Sequence 70, Appl
23	40	30.3	28	16	US-10-804-678-70	Sequence 70, Appl
24	39	29.5	27	9	US-09-887-855-8	Sequence 8, Appli
25	39	29.5	27	9	US-09-852-391-4	Sequence 4, Appli
26	39	29.5	27	10	US-09-876-790-12	Sequence 12, Appl
27	39	29.5	27	10	US-09-365-940-24	Sequence 24, Appl
28	39	29.5	27	14	US-10-158-238-13	Sequence 13, Appl
29	39	29.5	27	14	US-10-164-080-4	Sequence 4, Appli
30	39	29.5	27	14	US-10-242-212-4	Sequence 4, Appli
31	39	29.5	27	14	US-10-299-327-4	Sequence 4, Appli
32	39	29.5	27	14	US-10-200-242-24	Sequence 24, Appl
33	39	29.5	27	14	US-10-376-406-4	Sequence 4, Appli
34	39	29.5	27	15	US-10-200-242-24	Sequence 24, Appl
35	39	29.5	27	15	US-10-664-456-29	Sequence 29, Appl
36	39	29.5	27	15	US-10-652-244-14	Sequence 14, Appl
37	39	29.5	27	16	US-10-154-670-11	Sequence 11, Appl
38	39	29.5	27	17	US-10-888-779-12	Sequence 12, Appl
39	39	29.5	27	17	US-10-888-867-12	Sequence 12, Appl
40	39	29.5	27	17	US-10-888-780-12	Sequence 12, Appl
41	39	29.5	27	17	US-10-888-931-12	Sequence 12, Appl
42	38.5	29.2	25	16	US-10-416-249-163	Sequence 163, App
43	38	28.8	25	14	US-10-059-720-2	Sequence 2, Appli
44	38	28.8	26	14	US-10-059-720-3	Sequence 3, Appli
45	37	28.0	20	14	US-10-076-622-597	Sequence 597, App

ALIGNMENTS

RESULT 1
US-10-360-053-23
; Sequence 23, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenthal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibo
; TITLE OF INVENTION: Fragments via Antiparallel Hetergeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-23

Query Match 43.2%; Score 57; DB 14; Length 28;
Best Local Similarity 60.0%; Pred. No. 1.5;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 KIAALKQKIASLKQEIDALE 20
              | ||:| :||::|||| |:|
Db          5 KQAAIKNEIAAIKQEIAAIE 24
```

RESULT 2

US-10-360-053-22
; Sequence 22, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenthal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibo
; TITLE OF INVENTION: Fragments via Antiparallel Hetergeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-22

Query Match 40.9%; Score 54; DB 14; Length 28;
Best Local Similarity 55.0%; Pred. No. 3.8;
Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDALE 20
||||:::||| :::|| | |
Db 5 KIAAIEEKIAQIEEEIAAQE 24

RESULT 3
US-09-882-774-7
; Sequence 7, Application US/09882774
; Publication No. US20030021795A1
; GENERAL INFORMATION:
; APPLICANT: Houston, Michael E.
; APPLICANT: Hodges, Robert
; TITLE OF INVENTION: Use of Coiled-Coil Structural Scaffold to Generate
; TITLE OF INVENTION: Structure-Specific Peptides
; FILE REFERENCE: 003592-007
; CURRENT APPLICATION NUMBER: US/09/882,774
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,892
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/213,387
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hybrid sequence
; NAME/KEY: MOD_RES
; LOCATION: (2)
; OTHER INFORMATION: Nle
US-09-882-774-7

Query Match 39.4%; Score 52; DB 10; Length 27;
Best Local Similarity 54.5%; Pred. No. 6.6;
Matches 12; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDALEYE 22
:| |||:|| | :|| || |
Db 4 EIEALKKKIEELSDKIDELEKE 25

RESULT 4
US-09-320-907B-6
; Sequence 6, Application US/09320907B
; Publication No. US20020198360A1
; GENERAL INFORMATION:
; APPLICANT: GINSBERG, MARK H.
; APPLICANT: PFAFF, MARTIN
; TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; FILE REFERENCE: SRI-0006
; CURRENT APPLICATION NUMBER: US/09/320,907B
; CURRENT FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/187,236
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-320-907B-6

Query Match 38.6%; Score 51; DB 9; Length 28;
Best Local Similarity 40.7%; Pred. No. 9.2;
Matches 11; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDALEYENDALE 27
|: ||: :: :|: :::||| : ||||
Db 1 KLEALEGRLDALEGKLEALEGKLDALE 27

RESULT 5
US-10-447-292-6
; Sequence 6, Application US/10447292
; Publication No. US20030224453A1
; GENERAL INFORMATION:
; APPLICANT: GINSBERG, MARK H.
; APPLICANT: PFAFF, MARTIN
; TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; FILE REFERENCE: SRI-0006
; CURRENT APPLICATION NUMBER: US/10/447,292
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/320,907B
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/187,236
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-10-447-292-6

Query Match 38.6%; Score 51; DB 15; Length 28;
Best Local Similarity 40.7%; Pred. No. 9.2;
Matches 11; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDALEYENDALE 27
|: ||: :: :|: :::||| : ||||
Db 1 KLEALEGRLDALEGKLEALEGKLDALE 27

RESULT 6
US-09-259-658-59
; Sequence 59, Application US/09259658
; Publication No. US20030032054A1
; GENERAL INFORMATION:
; APPLICANT: Colyer

; APPLICANT: Craig
; APPLICANT: Maschio
; APPLICANT: Mezna
; TITLE OF INVENTION: Compositions And Methods For Monitoring The
; TITLE OF INVENTION: Modification State Of A Pair Of Polypeptides
; FILE REFERENCE: colyer 4256/79245
; CURRENT APPLICATION NUMBER: US/09/259,658
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: peptide used to assay geranylgeranyl transferase
; OTHER INFORMATION: activity.
US-09-259-658-59

Query Match 37.9%; Score 50; DB 10; Length 23;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEI 16
||| |||| | |||:|
Db 7 KIAQLKQKNACLKQKI 22

RESULT 7
US-10-338-083-19
; Sequence 19, Application US/10338083
; Publication No. US20030166559A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: coiled-coil motif
US-10-338-083-19

Query Match 34.8%; Score 46; DB 14; Length 24;
Best Local Similarity 41.7%; Pred. No. 34;
Matches 10; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 3 AALKQKIASLKQEIDALEYENDAL 26
|||: ::::|: |: :|| | ||
Db 1 AALESEVSALESEVASLESEVAAL 24

RESULT 8
US-10-611-399-19
; Sequence 19, Application US/10611399
; Publication No. US20040170602A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF
; FILE REFERENCE: A-71273-3
; CURRENT APPLICATION NUMBER: US/10/611,399
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: coiled-coil motif
US-10-611-399-19

Query Match 34.8%; Score 46; DB 16; Length 24;
Best Local Similarity 41.7%; Pred. No. 34;
Matches 10; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 3 AALKQKIASLKQEIDALEYENDAL 26
|||: ::::|: |: :|| | ||
Db 1 AALESEVSALESEVASLESEVAAL 24

RESULT 9
US-10-794-751-19
; Sequence 19, Application US/10794751
; Publication No. US20050048626A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Thomason, Adam Read
; APPLICANT: Zhukovsky, Eugene Alexander
; TITLE OF INVENTION: BAFF VARIANTS AND METHODS THEREOF
; FILE REFERENCE: A-72175-1
; CURRENT APPLICATION NUMBER: US/10/794,751
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/452,707
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/482,081
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 60/523,880
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US 60/528,104
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: coiled-coil motif
US-10-794-751-19

Query Match 34.8%; Score 46; DB 17; Length 24;
Best Local Similarity 41.7%; Pred. No. 34;
Matches 10; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 3 AALKQKIASLKQEIDALEYENDAL 26
|||: ::::|: |: :|| | ||
Db 1 AALESEVSALESEVASLESEVAAL 24

RESULT 10
US-10-360-053-21
; Sequence 21, Application US/10360053
; Publication No. US20030170230A1

```
; GENERAL INFORMATION:
;  APPLICANT: Caterer, Nigel
;  APPLICANT:  Uttenthal, Lars O
;  APPLICANT:  Nielsen, Rasmus W
;  TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibo
;  TITLE OF INVENTION:  Fragments via Antiparallel Hetergeneous Coiled-Coil Peptide Regi
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: IMX-0028
;  CURRENT APPLICATION NUMBER: US/10/360,053
;  CURRENT FILING DATE:  2003-02-05
;  PRIOR APPLICATION NUMBER: US60/354,376
;  PRIOR FILING DATE: 2002-02-05
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-360-053-21

  Query Match             34.1%;  Score 45;  DB 14;  Length 28;
  Best Local Similarity   56.2%;  Pred. No. 55;
  Matches    9;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEI 16
              :|||:| |||::|: |
Db         12 EIAAIKDKIAAIKEYI 27


RESULT 11
US-10-338-083-20
; Sequence 20, Application US/10338083
; Publication No. US20030166559A1
; GENERAL INFORMATION:
;  APPLICANT: Desjarlais, John R.
;  APPLICANT:  Tansey, Malu Lourdes G.
;  APPLICANT:  Dahiyat, Bassil I.
;  TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
;  FILE REFERENCE: A-71273-2
;  CURRENT APPLICATION NUMBER: US/10/338,083
;  CURRENT FILING DATE:  2003-01-16
;  PRIOR APPLICATION NUMBER: US 60/345,805
;  PRIOR FILING DATE: 2002-01-04
;  PRIOR APPLICATION NUMBER: US 60/373,453
;  PRIOR FILING DATE: 2002-04-17
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 24
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: coiled-coil motif
US-10-338-083-20

  Query Match             33.3%;  Score 44;  DB 14;  Length 24;
  Best Local Similarity   44.4%;  Pred. No. 62;
  Matches    8;  Conservative    7;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDA 18
              |::|:| |:||:| :: |
Db          7 KLSAVKSKLASVKSKLAA 24


RESULT 12
US-10-611-399-20
; Sequence 20, Application US/10611399
; Publication No. US20040170602A1
; GENERAL INFORMATION:
;  APPLICANT: Desjarlais, John R.
;  APPLICANT:  Tansey, Malu Lourdes G.
;  APPLICANT:  Dahiyat, Bassil I.
;  TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF
;  FILE REFERENCE: A-71273-3
;  CURRENT APPLICATION NUMBER: US/10/611,399
;  CURRENT FILING DATE:  2003-07-01
;  PRIOR APPLICATION NUMBER: US 10/338,083
;  PRIOR FILING DATE: 2003-01-06
;  PRIOR APPLICATION NUMBER: US 60/345,805
;  PRIOR FILING DATE: 2002-01-04
;  PRIOR APPLICATION NUMBER: US 60/373,453
;  PRIOR FILING DATE: 2002-04-17
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 24
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: coiled-coil motif
US-10-611-399-20

  Query Match             33.3%;  Score 44;  DB 16;  Length 24;
  Best Local Similarity   44.4%;  Pred. No. 62;
  Matches    8;  Conservative    7;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDA 18
              |::|:| |:||:| :: |
Db          7 KLSAVKSKLASVKSKLAA 24


RESULT 13
US-10-794-751-20
; Sequence 20, Application US/10794751
; Publication No. US20050048626A1
; GENERAL INFORMATION:
;  APPLICANT: Desjarlais, John R.
;  APPLICANT:  Thomason, Adam Read
;  APPLICANT:  Zhukovsky, Eugene Alexander
;  TITLE OF INVENTION: BAFF VARIANTS AND METHODS THEREOF
;  FILE REFERENCE: A-72175-1
;  CURRENT APPLICATION NUMBER: US/10/794,751
;  CURRENT FILING DATE:  2004-03-05
;  PRIOR APPLICATION NUMBER: US 10/338,083
;  PRIOR FILING DATE: 2003-01-06
;  PRIOR APPLICATION NUMBER: US 60/452,707
;  PRIOR FILING DATE: 2003-03-07
;  PRIOR APPLICATION NUMBER: US 60/482,081
;  PRIOR FILING DATE: 2003-06-23
;  PRIOR APPLICATION NUMBER: US 60/523,880
;  PRIOR FILING DATE: 2003-11-20
;  PRIOR APPLICATION NUMBER: US 60/528,104
;  PRIOR FILING DATE: 2003-12-08
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
;   LENGTH: 24
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: coiled-coil motif
US-10-794-751-20

  Query Match             33.3%;  Score 44;  DB 17;  Length 24;
  Best Local Similarity   44.4%;  Pred. No. 62;
  Matches    8;  Conservative    7;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDA 18
              |::|:| |:||:| :: |
Db          7 KLSAVKSKLASVKSKLAA 24


RESULT 14
US-10-630-926-7
```

```
; Sequence 7, Application US/10630926
; Publication No. US20040194160A1
;  GENERAL INFORMATION:
;       APPLICANT: RICCARDI, Carlo
;       TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL
;                           DEATH PATHWAYS
;       NUMBER OF SEQUENCES: 15
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
;            STREET: 624 Ninth Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/630,926
;            FILING DATE: 31-Jul-2003
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/403,861A
;            FILING DATE: 11-Feb-2000
;            APPLICATION NUMBER: PCT/EP98/02490
;            FILING DATE: 27-APR-1998
;            APPLICATION NUMBER: EP 97107033.9
;            FILING DATE: 28-APR-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: YUN, Allen C.
;            REGISTRATION NUMBER: 37,971
;            REFERENCE/DOCKET NUMBER: RICCARDI=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 26 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: pepetide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-630-926-7

  Query Match             33.3%;  Score 44;  DB 16;  Length 26;
  Best Local Similarity   43.5%;  Pred. No. 68;
  Matches   10;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          5 LKQKIASLKQEIDALEYENDALE 27
              ||::|  | ::   || ||| |:
Db          1 LKEQIKELIEKNSQLEQENDLLK 23


RESULT 15
US-09-834-759-534
; Sequence 534, Application US/09834759
; Publication No. US20020085998A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C9
;  CURRENT APPLICATION NUMBER: US/09/834,759
;  CURRENT FILING DATE:  2001-04-13
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 534
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-759-534

  Query Match             31.1%;  Score 41;  DB 9;  Length 21;
  Best Local Similarity   50.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 LKQKIASLKQEIDALEYE 22
              ||::|| || ||  |:::
Db          4 LKKEIAMLKLEIATLKHQ 21


Search completed: April 27, 2005, 15:22:47
Job time : 95.5 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2005, 14:58:17 ; Search time 29.5 Seconds
(without alignments)
70.853 Million cell updates/sec

Title: US-10-088-417A-1
Perfect score: 132
Sequence: 1 KIAALKQKIASLKQEIDALEYENDALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 228236

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	52	39.4	25	4	US-09-491-614B-25	Sequence 25, Appl
2	46	34.8	24	2	US-08-491-527A-12	Sequence 12, Appl
3	46	34.8	28	1	US-08-182-175A-1	Sequence 1, Appli
4	46	34.8	28	5	PCT-US92-06412-1	Sequence 1, Appli
5	45	34.1	24	2	US-08-491-527A-11	Sequence 11, Appl
6	44	33.3	26	4	US-09-403-861A-7	Sequence 7, Appli
7	41	31.1	21	4	US-09-834-759-534	Sequence 534, App
8	40	30.3	28	1	US-08-182-175A-3	Sequence 3, Appli
9	40	30.3	28	1	US-08-474-633A-70	Sequence 70, Appl
10	40	30.3	28	4	US-08-823-771-70	Sequence 70, Appl
11	40	30.3	28	5	PCT-US92-06412-3	Sequence 3, Appli
12	39	29.5	25	3	US-08-737-629-8	Sequence 8, Appli
13	39	29.5	27	1	US-08-446-922-9	Sequence 9, Appli
14	39	29.5	27	2	US-08-484-624A-24	Sequence 24, Appl
15	39	29.5	27	2	US-08-477-733B-24	Sequence 24, Appl
16	39	29.5	27	3	US-09-088-913A-24	Sequence 24, Appl
17	39	29.5	27	3	US-08-737-629-1	Sequence 1, Appli
18	39	29.5	27	3	US-08-769-819-24	Sequence 24, Appl
19	39	29.5	27	3	US-09-320-424-14	Sequence 14, Appl
20	39	29.5	27	3	US-08-770-974-24	Sequence 24, Appl
21	39	29.5	27	3	US-08-770-981-24	Sequence 24, Appl
22	39	29.5	27	4	US-09-399-106-24	Sequence 24, Appl
23	39	29.5	27	4	US-09-645-926A-4	Sequence 4, Appli
24	39	29.5	27	4	US-09-509-802-4	Sequence 4, Appli
25	39	29.5	27	4	US-09-825-563-14	Sequence 14, Appl
26	39	29.5	27	4	US-09-852-391-4	Sequence 4, Appli
27	39	29.5	27	4	US-09-524-100C-12	Sequence 12, Appl
28	39	29.5	27	4	US-09-976-472A-4	Sequence 4, Appli
29	38	28.8	25	2	US-08-690-011A-2	Sequence 2, Appli
30	38	28.8	25	3	US-09-299-495F-2	Sequence 2, Appli
31	38	28.8	26	2	US-08-690-011A-3	Sequence 3, Appli
32	38	28.8	26	3	US-09-299-495F-3	Sequence 3, Appli
33	37	28.0	26	2	US-08-690-011A-37	Sequence 37, Appl
34	37	28.0	26	3	US-09-299-495F-37	Sequence 37, Appl
35	37	28.0	27	4	US-09-664-945-77	Sequence 77, Appl
36	37	28.0	28	1	US-08-182-175A-2	Sequence 2, Appli
37	37	28.0	28	1	US-08-182-175A-39	Sequence 39, Appl
38	37	28.0	28	1	US-08-182-175A-43	Sequence 43, Appl
39	37	28.0	28	1	US-08-182-175A-47	Sequence 47, Appl
40	37	28.0	28	1	US-08-474-633A-36	Sequence 36, Appl
41	37	28.0	28	1	US-08-474-633A-40	Sequence 40, Appl
42	37	28.0	28	1	US-08-474-633A-56	Sequence 56, Appl
43	37	28.0	28	1	US-08-474-633A-67	Sequence 67, Appl
44	37	28.0	28	1	US-08-944-133-18	Sequence 18, Appl
45	37	28.0	28	1	US-08-944-133-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-491-614B-25
; Sequence 25, Application US/09491614B
; Patent No. 6828106
; GENERAL INFORMATION:
; APPLICANT: Colyer, John
; TITLE OF INVENTION: Methods and Compositions Using Coiled Binding Partners
; FILE REFERENCE: 10069/1150
; CURRENT APPLICATION NUMBER: US/09/491,614B
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 09/259,474
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 25
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Peptide for forming a coiled coil
; FEATURE:
; NAME/KEY: Acetylation
; LOCATION: (1)..(1)
; FEATURE:
; NAME/KEY: Amidation
; LOCATION: (25)..(25)
US-09-491-614B-25

Query Match 39.4%; Score 52; DB 4; Length 25;
Best Local Similarity 60.0%; Pred. No. 0.69;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```
Qy          9 IASLKQEIDALEYENDALEQ 28
              ||:|::||  || ||  |||
Db          1 IAALEREIYKLEQENQQLEQ 20
```

RESULT 2
US-08-491-527A-12
; Sequence 12, Application US/08491527A
; Patent No. 5824483
; GENERAL INFORMATION:
; APPLICANT: Houston, Michael E.
; APPLICANT: Hodges, Robert S.
; TITLE OF INVENTION: Conformationally-Restricted Combinatorial
; TITLE OF INVENTION: Library Composition and Method
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250

```
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/491,527A
;      FILING DATE:  16-JUNE-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/260,199
;      FILING DATE:  15-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/245,507
;      FILING DATE:  18-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sholtz, Charles K.
;      REGISTRATION NUMBER:  38,615
;      REFERENCE/DOCKET NUMBER:  7900-0008.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  LPS epitope library peptide, Fig. 5A
US-08-491-527A-12

  Query Match             34.8%;  Score 46;  DB 2;  Length 24;
  Best Local Similarity   54.5%;  Pred. No. 4.6;
  Matches   12;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALEYE 22
              :| |||::|  | |:| ||| |
Db          1 EIEALKKEIHFLVQKIHALEKE 22


RESULT 3
US-08-182-175A-1
; Sequence 1, Application US/08182175A
; Patent No. 5559223
;  GENERAL INFORMATION:
;    APPLICANT:  Saverio Carl Falco
;    APPLICANT:  Sharon J. Keeler
;    APPLICANT:  Janet A. Rice
;    TITLE OF INVENTION:  Synthetic Storage Proteins with Defined Structure Containing P
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E.I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh System, 6.0
;      SOFTWARE:  Microsoft Word, 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/182,175A
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/743,006
;      FILING DATE:  9 August 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Linda Axamethy Floyd
;      REGISTRATION NUMBER:  33,692
;      REFERENCE/DOCKET NUMBER:  BB-1031
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (302) 992-4929
;      TELEFAX:  (302) 892-7949
;      TELEX:  835420
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..28
;      OTHER INFORMATION:  /label= name
;      OTHER INFORMATION:  /note= "(SSP 4)4"
US-08-182-175A-1

  Query Match             34.8%;  Score 46;  DB 1;  Length 28;
  Best Local Similarity   40.0%;  Pred. No. 5.5;
  Matches    8;  Conservative    9;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALE 20
              |: ||::|: :|:::: |||
Db          4 KLKALEEKLKALEEKLKALE 23


RESULT 4
PCT-US92-06412-1
; Sequence 1, Application PC/TUS9206412
;  GENERAL INFORMATION:
;    APPLICANT:  Saverio Carl Falco
;    APPLICANT:  Sharon J. Keeler
;    APPLICANT:  Janet A. Rice
;    TITLE OF INVENTION:  Synthetic Storage Proteins with Defined Structure Containing P
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E.I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh System, 6.0
;      SOFTWARE:  Microsoft Word, 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/06412
;      FILING DATE:  19920807
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/743,006
;      FILING DATE:  9 August 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Linda Axamethy Floyd
;      REGISTRATION NUMBER:  33,692
;      REFERENCE/DOCKET NUMBER:  BB-1031
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (302) 992-4929
;      TELEFAX:  (302) 892-7949
;      TELEX:  835420
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
```

```
;       TYPE:  AMINO ACID
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  Protein
;       LOCATION:  1..28
;       OTHER INFORMATION:  /label= name
;       OTHER INFORMATION:  /note= "(SSP 4)4"
PCT-US92-06412-1

  Query Match            34.8%;  Score 46;  DB 5;  Length 28;
  Best Local Similarity  40.0%;  Pred. No. 5.5;
  Matches    8;  Conservative    9;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALE 20
              |: ||::|: :|:::: |||
Db          4 KLKALEEKLKALEEKLKALE 23


RESULT 5
US-08-491-527A-11
; Sequence 11, Application US/08491527A
; Patent No. 5824483
;  GENERAL INFORMATION:
;    APPLICANT:  Houston, Michael E.
;    APPLICANT:  Hodges, Robert S.
;    TITLE OF INVENTION:  Conformationally-Restricted Combinatorial
;    TITLE OF INVENTION:  Library Composition and Method
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/491,527A
;      FILING DATE:  16-JUNE-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/260,199
;      FILING DATE:  15-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/245,507
;      FILING DATE:  18-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sholtz, Charles K.
;      REGISTRATION NUMBER:  38,615
;      REFERENCE/DOCKET NUMBER:  7900-0008.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  exemplary generic library peptide,
;      INDIVIDUAL ISOLATE:  Fig. 3A
US-08-491-527A-11

  Query Match            34.1%;  Score 45;  DB 2;  Length 24;
  Best Local Similarity  50.0%;  Pred. No. 6.3;
  Matches   11;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALEYE 22
              :| |||::|  |  :| ||| |
Db          1 EIEALKKEIXXLXXKIXALEKE 22


RESULT 6
US-09-403-861A-7
; Sequence 7, Application US/09403861A
; Patent No. 6833348
;  GENERAL INFORMATION:
;       APPLICANT: RICCARDI, Carlo
;       TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL
;                           DEATH PATHWAYS
;       NUMBER OF SEQUENCES: 15
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
;            STREET: 624 Ninth Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/403,861A
;            FILING DATE: 11-Feb-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/EP98/02490
;            FILING DATE: 27-APR-1998
;            APPLICATION NUMBER: EP 97107033.9
;            FILING DATE: 28-APR-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: YUN, Allen C.
;            REGISTRATION NUMBER: 37,971
;            REFERENCE/DOCKET NUMBER: RICCARDI=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 26 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: pepetide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-403-861A-7

  Query Match            33.3%;  Score 44;  DB 4;  Length 26;
  Best Local Similarity  43.5%;  Pred. No. 9.6;
  Matches   10;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          5 LKQKIASLKQEIDALEYENDALE 27
              ||::|  | ::   || ||| |:
Db          1 LKEQIKELIEKNSQLEQENDLLK 23


RESULT 7
US-09-834-759-534
; Sequence 534, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
```

```
;  APPLICANT:  Henderson, Robert A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C9
;  CURRENT APPLICATION NUMBER: US/09/834,759
;  CURRENT FILING DATE:  2001-04-13
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 534
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-759-534

  Query Match             31.1%;  Score 41;  DB 4;  Length 21;
  Best Local Similarity   50.0%;  Pred. No. 20;
  Matches    9;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 LKQKIASLKQEIDALEYE 22
              ||::|| || ||  |:::
Db          4 LKKEIAMLKLEIATLKHQ 21


RESULT 8
US-08-182-175A-3
; Sequence 3, Application US/08182175A
; Patent No. 5559223
;  GENERAL INFORMATION:
;    APPLICANT:  Saverio Carl Falco
;    APPLICANT:  Sharon J. Keeler
;    APPLICANT:  Janet A. Rice
;    TITLE OF INVENTION:  Synthetic Storage Proteins with Defined Structure Containing E
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E.I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh System, 6.0
;      SOFTWARE:  Microsoft Word, 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/182,175A
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/743,006
;      FILING DATE:  9 August 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Linda Axamethy Floyd
;      REGISTRATION NUMBER:  33,692
;      REFERENCE/DOCKET NUMBER:  BB-1031
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (302) 992-4929
;      TELEFAX:  (302) 892-7949
;      TELEX:  835420
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..28
;      OTHER INFORMATION:  /label= name
;      OTHER INFORMATION:  /note= "(SSP 7)4"
US-08-182-175A-3

  Query Match             30.3%;  Score 40;  DB 1;  Length 28;
  Best Local Similarity   25.0%;  Pred. No. 38;
  Matches    5;  Conservative   12;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALE 20
              |: |:::|: :::::: |:|
Db          4 KLKAMEEKLKAMEEKLKAME 23


RESULT 9
US-08-474-633A-70
; Sequence 70, Application US/08474633A
; Patent No. 5773691
;  GENERAL INFORMATION:
;    APPLICANT:  E. I. DU PONT DE NEMOURS AND
;    APPLICANT:  COMPANY
;    TITLE OF INVENTION:  CHIMERIC GENES AND
;    TITLE OF INVENTION:  METHODS FOR INCREASING
;    TITLE OF INVENTION:  INCREASING THE LYSINE
;    TITLE OF INVENTION:  AND THREONINE CONTENT
;    TITLE OF INVENTION:  OF THE SEEDS OF PLANTS
;    NUMBER OF SEQUENCES:  107
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. DU PONT DE NEMOURS
;      ADDRESSEE:  AND COMPANY
;      STREET:  1007 MARKET STREET
;      CITY:  WILMINGTON
;      STATE:  DELAWARE
;      COUNTRY:  U.S.A.
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MICROSOFT WORD VERSION 2.0C
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,633A
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BARBARA C. SIEGELL
;      REGISTRATION NUMBER:  30,684
;      REFERENCE/DOCKET NUMBER:  BB-1037-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4931
;      TELEFAX:  302-773-0164
;      TELEX:  835420
;  INFORMATION FOR SEQ ID NO:  70:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..28
;      OTHER INFORMATION:  /label= name
;      OTHER INFORMATION:  /note= "(SSP 7)4"
US-08-474-633A-70

  Query Match             30.3%;  Score 40;  DB 1;  Length 28;
  Best Local Similarity   25.0%;  Pred. No. 38;
  Matches    5;  Conservative   12;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALE 20
              |: |:::|: :::::: |:|
Db          4 KLKAMEEKLKAMEEKLKAME 23


RESULT 10
US-08-823-771-70
```

```
; Sequence 70, Application US/08823771
; Patent No. 6459019
;  GENERAL INFORMATION:
;       APPLICANT: E. I. DU PONT DE NEMOURS AND
;                  COMPANY
;       TITLE OF INVENTION: CHIMERIC GENES AND
;                           METHODS FOR INCREASING
;                           INCREASING THE LYSINE
;                           AND THREONINE CONTENT
;       NUMBER OF SEQUENCES: 107
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: E. I. DU PONT DE NEMOURS
;                       AND COMPANY
;            STREET: 1007 MARKET STREET
;            CITY: WILMINGTON
;            STATE: DELAWARE
;            COUNTRY: U.S.A.
;            ZIP: 19898
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: FLOPPY DISK
;            COMPUTER: IBM PC COMPATIBLE
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: MICROSOFT WORD VERSION 2.0C
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/823,771
;            FILING DATE: 24-Mar-1997
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/474,633
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BARBARA C. SIEGELL
;            REGISTRATION NUMBER: 30,684
;            REFERENCE/DOCKET NUMBER: BB-1037-C
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 302-992-4931
;            TELEFAX: 302-773-0164
;            TELEX: 835420
;  INFORMATION FOR SEQ ID NO: 70:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 28 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: unknown
;            TOPOLOGY: unknown
;       MOLECULE TYPE: protein
;       FEATURE:
;            NAME/KEY:   Protein
;            LOCATION:   1..28
;            OTHER INFORMATION:   /label= name
;            /note= "(SSP 7)4"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-08-823-771-70

  Query Match             30.3%;  Score 40;  DB 4;  Length 28;
  Best Local Similarity   25.0%;  Pred. No. 38;
  Matches    5;  Conservative   12;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALE 20
              |: |:::|: :::::: |:|
Db          4 KLKAMEEKLKAMEEKLKAME 23


RESULT 11
PCT-US92-06412-3
; Sequence 3, Application PC/TUS9206412
;  GENERAL INFORMATION:
;    APPLICANT:  Saverio Carl Falco
;    APPLICANT:  Sharon J. Keeler
;    APPLICANT:  Janet A. Rice
;    TITLE OF INVENTION:  Synthetic Storage Proteins with Defined Structure Containing E
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E.I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh System, 6.0
;      SOFTWARE:  Microsoft Word, 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/06412
;      FILING DATE:  19920807
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/743,006
;      FILING DATE:  9 August 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Linda Axamethy Floyd
;      REGISTRATION NUMBER:  33,692
;      REFERENCE/DOCKET NUMBER:  BB-1031
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (302) 992-4929
;      TELEFAX:  (302) 892-7949
;      TELEX:  835420
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..28
;      OTHER INFORMATION:  /label= name
;      OTHER INFORMATION:  /note= "(SSP 7)4"
PCT-US92-06412-3

  Query Match             30.3%;  Score 40;  DB 5;  Length 28;
  Best Local Similarity   25.0%;  Pred. No. 38;
  Matches    5;  Conservative   12;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KIAALKQKIASLKQEIDALE 20
              |: |:::|: :::::: |:|
Db          4 KLKAMEEKLKAMEEKLKAME 23


RESULT 12
US-08-737-629-8
; Sequence 8, Application US/08737629
; Patent No. 6190886
;  GENERAL INFORMATION:
;    APPLICANT:  Hoppe, Hans-Jurgen
;    APPLICANT:  Reid, Kenneth BM
;    TITLE OF INVENTION:  Trimerising polypeptides, their manufacture
;    TITLE OF INVENTION:  and use.
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon & Vanderhye PC
;      STREET:  8th Floor, 1100 No. 6190886th Glebe Road
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  United States of America
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/737,629
;      FILING DATE:  10-JAN-1997
;      CLASSIFICATION:  435
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01104
;      FILING DATE:  16-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9409768.0
;      FILING DATE:  16-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ms Mary J Wilson
;      REGISTRATION NUMBER:  32,955
;      REFERENCE/DOCKET NUMBER:  620-10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 816-4000
;      TELEFAX:  (703) 816-4100
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-737-629-8

  Query Match             29.5%;  Score 39;  DB 3;  Length 25;
  Best Local Similarity   50.0%;  Pred. No. 46;
  Matches    6;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 IASLKQEIDALE 20
              :|||:|:::||:
Db          1 VASLRQQVEALQ 12


RESULT 13
US-08-446-922-9
; Sequence 9, Application US/08446922
; Patent No. 5716805
;  GENERAL INFORMATION:
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Srinivasan, Subhashini
;    TITLE OF INVENTION:  Methods of Preparing Soluble, Oligomeric
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,922
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/107,353
;      FILING DATE:  08-13-93
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia A
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  1003-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)233-0644
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-446-922-9

  Query Match             29.5%;  Score 39;  DB 1;  Length 27;
  Best Local Similarity   50.0%;  Pred. No. 51;
  Matches    6;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 IASLKQEIDALE 20
              :|||:|:::||:
Db          3 VASLRQQVEALQ 14


RESULT 14
US-08-484-624A-24
; Sequence 24, Application US/08484624A
; Patent No. 5962406
;  GENERAL INFORMATION:
;    APPLICANT:  ARMITAGE, RICHARD
;    APPLICANT:  FANSLOW, WILLIAM
;    APPLICANT:  SPRIGGS, MELANIE
;    APPLICANT:  SRINIVASAN, SUBHASHINI
;    APPLICANT:  GIBSON, MARYLOU
;    APPLICANT:  MORRIS, ARVIA E.
;    APPLICANT:  MCGREW, JEFFERY
;    TITLE OF INVENTION:  NOVEL CYTOKINE THAT BINDS CD40
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  MS Word for Apple Power Macintosh, version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,624A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/477,733
;      FILING DATE:  June 07, 1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/969,703
;      FILING DATE:  October 23, 1992
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/805,723
;      FILING DATE:  December 5, 1991
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/783,707
;      FILING DATE:  October 25, 1991
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia A.
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  2802-D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  2065870430
;      TELEFAX:  2065870606
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
```

```
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-484-624A-24

  Query Match             29.5%;  Score 39;  DB 2;  Length 27;
  Best Local Similarity   50.0%;  Pred. No. 51;
  Matches    6;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 IASLKQEIDALE 20
              :|||:|:::||:
Db          3 VASLRQQVEALQ 14


RESULT 15
US-08-477-733B-24
; Sequence 24, Application US/08477733B
; Patent No. 5981724
;  GENERAL INFORMATION:
;    APPLICANT:  ARMITAGE, RICHARD
;    APPLICANT:  FANSLOW, WILLIAM
;    APPLICANT:  SPRIGGS, MELANIE
;    APPLICANT:  SRINIVASAN, SUBHASHINI
;    APPLICANT:  GIBSON, MARYLOU
;    APPLICANT:  MORRIS, ARVIA E.
;    APPLICANT:  MCGREW, JEFFERY
;    TITLE OF INVENTION:  NOVEL CYTOKINE THAT BINDS CD40
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  MS Word for Apple Power Macintosh, version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,733B
;      FILING DATE:  June 07, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/249,189
;      FILING DATE:  May 24, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/969,703
;      FILING DATE:  October 23, 1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/805,723
;      FILING DATE:  December 5, 1991
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/783,707
;      FILING DATE:  October 25, 1991
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia A.
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  2802-D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  2065870430
;      TELEFAX:  2065870606
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-477-733B-24

  Query Match             29.5%;  Score 39;  DB 2;  Length 27;
  Best Local Similarity   50.0%;  Pred. No. 51;
  Matches    6;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 IASLKQEIDALE 20
              :|||:|:::||:
Db          3 VASLRQQVEALQ 14


Search completed: April 27, 2005, 15:19:42
Job time : 38.5 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2005, 14:54:59 ; Search time 23.5 Seconds
(without alignments)
114.641 Million cell updates/sec

Title: US-10-088-417A-1
Perfect score: 132
Sequence: 1 KIAALKQKIASLKQEIDALEYENDALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 5694

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	33	25.0	22	2	JP0069	ribosomal protein
2	33	25.0	25	2	S27229	prothymosin alpha
3	31	23.5	25	2	JP0067	ribosomal protein
4	30	22.7	20	2	A61276	superoxide dismuta
5	30	22.7	27	2	A38123	probable mauD prot
6	29	22.0	16	2	E58503	superoxide dismuta
7	29	22.0	21	2	F38837	T-cell receptor be
8	29	22.0	22	2	JP0066	ribosomal protein
9	28	21.2	18	2	A20923	light meromyosin -
10	28	21.2	23	2	PH0858	MauD protein - Par
11	27	20.5	21	2	I40659	hypothetical prote
12	27	20.5	21	2	I40657	hypothetical prote
13	27	20.5	25	2	A44790	probable colonizat
14	27	20.5	27	2	JP0065	ribosomal protein
15	27	20.5	28	2	A61417	bdellin B-3 - medi
16	26.5	20.1	26	2	F69265	hypothetical prote
17	26.5	20.1	27	2	S17646	alcohol dehydrogen
18	26	19.7	23	2	S24279	hypothetical prote
19	26	19.7	24	2	A43431	phosphorylase kina
20	26	19.7	25	2	A23605	histone H1.1 - whe
21	26	19.7	26	2	PL0027	M protein pepM19 -
22	26	19.7	27	2	I46492	myosin - rabbit (f
23	25.5	19.3	20	2	A53592	H+-exporting ATPas
24	25	18.9	14	2	A61032	troponin T, cardia
25	25	18.9	15	2	PA0025	protein QA300026 -
26	25	18.9	19	2	PN0467	nitrogenase (EC 1.
27	25	18.9	24	2	S47281	hypothetical prote
28	25	18.9	25	2	B44560	terephthalate 1,2-
29	25	18.9	28	2	PL0005	pepsin A (EC 3.4.2
30	24.5	18.6	20	2	S06149	photosystem I chai
31	24	18.2	15	2	PA0076	fructose-bisphosph
32	24	18.2	15	2	PA0071	superoxide dismuta
33	24	18.2	19	2	A38382	15K protein A - ra
34	24	18.2	20	2	B38382	15K protein B - ra
35	24	18.2	25	2	A30590	cytolytic enteroto
36	24	18.2	26	2	S70932	DNA-binding protei
37	24	18.2	27	1	QXASD	hypothetical prote
38	24	18.2	27	2	I50388	myosin heavy chain
39	24	18.2	28	2	A44877	cell surface prote
40	23	17.4	11	2	PH0914	T-cell receptor be
41	23	17.4	12	2	PH1605	Ig H chain V-D-J r
42	23	17.4	13	2	S65612	tubulin alpha-chai
43	23	17.4	14	1	QMVHMM	mastoparan M - hor
44	23	17.4	14	1	QMWAVV	mastoparan - yello
45	23	17.4	14	2	JN0389	histamine-releasin

ALIGNMENTS

RESULT 1
JP0069
ribosomal protein L30 - Thermomonospora mesophila (fragment)
C;Species: Thermomonospora mesophila
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
C;Accession: JP0069
R;Ochi, K.
submitted to JIPID, February 1994
A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr
A;Reference number: JP0042
A;Accession: JP0069
A;Molecule type: protein
A;Residues: 1-22 <OCH>
C;Keywords: protein biosynthesis; ribosome

Query Match 25.0%; Score 33; DB 2; Length 22;
Best Local Similarity 36.8%; Pred. No. 5e+02;
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

```
Qy          1 KIAALKQKIASLKQEIDAL 19
              ||  |: ||   : : | |
Db          4 KITQLRSKIGGKQNQXDXL 22
```

RESULT 2
S27229
prothymosin alpha homolog - Escherichia coli (fragments)
C;Species: Escherichia coli
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S27229
R;Vartapetian, A.; Chichkova, N.; Lyakhov, I.; Makarova, T.; Evstafieva, A.; Bogdanov, A
FEBS Lett. 313, 95-97, 1992
A;Title: Segments of Escherichia coli genome similar to the exons of human prothymosin a
A;Reference number: S27229; MUID:93050251; PMID:1426289
A;Accession: S27229
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-6;7-25 <VAR>
A;Note: the authors did not translate the codon for residues 17

Query Match 25.0%; Score 33; DB 2; Length 25;
Best Local Similarity 42.1%; Pred. No. 5.8e+02;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```
Qy         10 ASLKQEIDALEYENDALEQ 28
              ||: :|   || :||  |:
Db          4 ASVNEENGELEADNDDDEE 22
```

RESULT 3
JP0067
ribosomal protein L30 - Thermomonospora chromogena (fragment)

C;Species: Thermomonospora chromogena
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
C;Accession: JP0067
R;Ochi, K.
submitted to JIPID, February 1994
A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr
A;Reference number: JP0042
A;Accession: JP0067
A;Molecule type: protein
A;Residues: 1-25 <OCH>
C;Keywords: protein biosynthesis; ribosome

Query Match 23.5%; Score 31; DB 2; Length 25;
Best Local Similarity 31.6%; Pred. No. 1e+03;
Matches 6; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDAL 19
Db 4 KITQVRSKIGGKQNQXDSL 22

RESULT 4
A61276
superoxide dismutase (EC 1.15.1.1) (Fe/Mn) homolog - chicken (fragment)
N;Alternate names: osteoclast membrane glycoprotein
C;Species: Gallus gallus (chicken)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 05-Mar-1999
C;Accession: A61276
R;Oursler, M.J.; Li, L.; Osdoby, P.
J. Cell. Biochem. 46, 219-233, 1991
A;Title: Purification and characterization of an osteoclast membrane glycoprotein with h
A;Reference number: A61276; MUID:92129474; PMID:1723067
A;Accession: A61276
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <OUR>
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Keywords: metalloprotein; oxidoreductase

Query Match 22.7%; Score 30; DB 2; Length 20;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 15 EIDALEYENDALE 27
Db 3 ELPDLPYAYDALE 15

RESULT 5
A38123
probable mauD protein - Methylobacterium extorquens (strain AM1) (fragment)
C;Species: Methylobacterium extorquens
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004
C;Accession: A38123
R;Chistoserdov, A.Y.; Lidstrom, M.E.
J. Bacteriol. 173, 5909-5913, 1991
A;Title: The small-subunit polypeptide of methylamine dehydrogenase from Methylobacteriu
A;Reference number: A38123; MUID:91358386; PMID:1885555
A;Accession: A38123
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <CHI>
A;Cross-references: UNIPROT:Q49126; GB:M57963

Query Match 22.7%; Score 30; DB 2; Length 27;
Best Local Similarity 29.2%; Pred. No. 1.5e+03;
Matches 7; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 2 IAALKQKIASLKQEIDALEYENDA 25
Db 1 LEADKSGFASIQQFMTSRKHSHDA 24

RESULT 6
E58503
superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)
N;Alternate names: 21.3K bladder and kidney stone protein
C;Species: unidentified bacterium
C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C;Accession: E58503
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58501
A;Accession: E58503
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <BIN>
A;Cross-references: UNIPROT:Q7M137
A;Experimental source: human bladder and kidney stones
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Keywords: metalloprotein; oxidoreductase

Query Match 22.0%; Score 29; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 12 LKQEIDALEYENDAL 26
Db 1 MEHTLPPLPYEMDAL 15

RESULT 7
F38837
T-cell receptor beta chain precursor V region (23.1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 23-Jul-1999
C;Accession: F38837
R;Uematsu, Y.; Wege, H.; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayi, G.;
Proc. Natl. Acad. Sci. U.S.A. 88, 8534-8538, 1991
A;Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheumato
A;Reference number: A41299; MUID:92020887; PMID:1656449
A;Accession: F38837
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-21 <UEM>
A;Cross-references: GB:S57606; NID:g236346; PIDN:AAB19970.1; PID:g236347
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 22.0%; Score 29; DB 2; Length 21;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 12 LKQEIDALEYENDAL 26
Db 1 LSLNVNALELDDSAL 15

RESULT 8
JP0066
ribosomal protein L30 - Nocardia asteroides (fragment)
C;Species: Nocardia asteroides
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: JP0066
R;Ochi, K.
submitted to JIPID, February 1994
A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal p
A;Reference number: JP0042
A;Accession: JP0066
A;Molecule type: protein
A;Residues: 1-22 <OCH>
A;Cross-references: UNIPROT:Q7M0Z8
C;Keywords: protein biosynthesis; ribosome

```
  Query Match             22.0%;  Score 29;  DB 2;  Length 22;
  Best Local Similarity   31.6%;  Pred. No. 1.6e+03;
  Matches    6;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          8 KIASLKQEIDALEYENDAL 26
              |:  :|  | |   : d:|
Db          4 KVTQIKSTIGAKANQKDSL 22


RESULT 9
A20923
light meromyosin - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A20923
R;Nyitray, L.; Mocz, G.; Szilagyi, L.; Balint, M.; Lu, R.C.; Wong, A.; Gergely, J.
J. Biol. Chem. 258, 13213-13220, 1983
A;Title: The proteolytic substructure of light meromyosin.
A;Reference number: A92403; MUID:84032553; PMID:6355107
A;Accession: A20923
A;Molecule type: protein
A;Residues: 1-18 <NYI>
A;Cross-references: UNIPROT:Q8JG72
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP; muscle

  Query Match             21.2%;  Score 28;  DB 2;  Length 18;
  Best Local Similarity   35.7%;  Pred. No. 1.7e+03;
  Matches    5;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 ALKQKIASLKQEID 17
              |  |:|  ||::::
Db          4 AFTQQIEELKRQLE 17


RESULT 10
PH0858
MauD protein - Paracoccus denitrificans (fragment)
C;Species: Paracoccus denitrificans
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
C;Accession: PH0858
R;Chistoserdov, A.Y.; Boyd, J.; Mathews, F.S.; Lidstrom, M.E.
Biochem. Biophys. Res. Commun. 184, 1181-1189, 1992
A;Title: The genetic organization of the mau gene cluster of the facultative autotroph P
A;Reference number: PH0856; MUID:92272706; PMID:1590782
A;Accession: PH0858
A;Molecule type: DNA
A;Residues: 1-23 <CHI>
A;Cross-references: UNIPROT:P29895; GB:M90098; NID:g150580; PIDN:AAA25577.1; PID:g150581
C;Genetics:
A;Gene: mauD

  Query Match             21.2%;  Score 28;  DB 2;  Length 23;
  Best Local Similarity   46.2%;  Pred. No. 2.2e+03;
  Matches    6;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 AALKQKIASLKQE 15
              |:|:|  :|| |::
Db          9 ASLQQYMASRKKQ 21


RESULT 11
I40659
hypothetical protein - Clostridium cochlearium (fragment)
C;Species: Clostridium cochlearium
C;Date: 12-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C;Accession: I40659; S47461
R;Zelder, O.; Beatrix, B.; Leutbecher, U.; Buckel, W.
Eur. J. Biochem. 226, 577-585, 1994
A;Title: Characterization of the coenzyme-B12-dependent glutamate mutase from Clostridiu
A;Reference number: I40659; MUID:95094816; PMID:7880251
A;Accession: I40659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-21 <RES>
A;Cross-references: UNIPROT:Q46011; EMBL:X80997; NID:g530005; PIDN:CAA56920.1; PID:g5300

  Query Match             20.5%;  Score 27;  DB 2;  Length 21;
  Best Local Similarity   41.7%;  Pred. No. 2.7e+03;
  Matches    5;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IAALKQKIASLK 13
              : ||| |:  :|
Db          7 VKALKSKLLEVK 18


RESULT 12
I40657
hypothetical protein 21 - Clostridium cochlearium (fragment)
C;Species: Clostridium cochlearium
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40657; S41331
R;Zelder, O.; Beatrix, B.; Buckel, W.
FEMS Microbiol. Lett. 118, 15-21, 1994
A;Title: Cloning, sequencing and expression in Escherichia coli of the gene encoding co
A;Reference number: I40657; MUID:94283856; PMID:8013871
A;Accession: I40657
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-21 <RES>
A;Cross-references: UNIPROT:Q46010; EMBL:X75890; NID:g441487; PIDN:CAA53483.1; PID:g4414

  Query Match             20.5%;  Score 27;  DB 2;  Length 21;
  Best Local Similarity   41.7%;  Pred. No. 2.7e+03;
  Matches    5;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IAALKQKIASLK 13
              : ||| |:  :|
Db          7 VKALKSKLLEVK 18


RESULT 13
A44790
probable colonization factor O166 - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 24-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44790
R;Sommerfelt, H.; Grewal, H.M.; Svennerholm, A.M.; Gaastra, W.; Flood, P.R.; Viboud, G.,
Infect. Immun. 60, 3799-3806, 1992
A;Title: Genetic relationship of putative colonization factor O166 to colonization facto
A;Reference number: A44790; MUID:92363580; PMID:1354200
A;Contents: E7476A
A;Accession: A44790
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-25 <SOM>
A;Cross-references: UNIPROT:Q9R5J4
A;Note: sequence extracted from NCBI backbone (NCBIP:111010)
C;Superfamily: CFA1 fimbrial protein

  Query Match             20.5%;  Score 27;  DB 2;  Length 25;
  Best Local Similarity   41.2%;  Pred. No. 3.2e+03;
  Matches    7;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         10 ASLKQEIDALEYENDAL 26
              ||:   || |:    ||
Db          9 ASVDPTIDILQANGSAL 25


RESULT 14
JP0065
ribosomal protein L30 - Streptomyces rochei (fragment)
C;Species: Streptomyces rochei
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 21-Aug-1998
C;Accession: JP0065
```

R;Ochi, K.
submitted to JIPID, February 1994
A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr
A;Reference number: JP0042
A;Accession: JP0065
A;Molecule type: protein
A;Residues: 1-27 <OCH>
C;Superfamily: Escherichia coli ribosomal protein L30
C;Keywords: protein biosynthesis; ribosome

Query Match 20.5%; Score 27; DB 2; Length 27;
Best Local Similarity 36.8%; Pred. No. 3.5e+03;
Matches 7; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDAL 19
|| :| | | : | |
Db 4 KITQVKSYIGSKQNXXDTL 22

RESULT 15
A61417
bdellin B-3 - medicinal leech (fragment)
C;Species: Hirudo medicinalis (medicinal leech)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
C;Accession: A61417
R;Krejci, K.; Fritz, H.
FEBS Lett. 64, 152-155, 1976
A;Title: Structural homology of a trypsin-plasmin inhibitor from leeches (bdellin B-3) w
A;Reference number: A61417; MUID:76188026; PMID:131707
A;Accession: A61417
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <KRE>

Query Match 20.5%; Score 27; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 17 DALEYENDAL 26
| : |:|: |
Db 17 DGVTYDNECL 26

Search completed: April 27, 2005, 15:07:07
Job time : 29.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2005, 14:46:25 ; Search time 112 Seconds
(without alignments)
128.020 Million cell updates/sec

Title: US-10-088-417A-1
Perfect score: 132
Sequence: 1 KIAALKQKIASLKQEIDALEYENDALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 23310

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	28.8	20	1	SODF_PASPI	P81527 pasteurella
2	38	28.8	23	2	Q9UCS1	Q9ucs1 homo sapien
3	35	26.5	26	2	Q7RR69	Q7rr69 plasmodium
4	34	25.8	22	2	O44710	O44710 drosophila
5	32	24.2	16	2	Q95Y34	Q95y34 caenorhabdi
6	32	24.2	28	2	Q8ZYY3	Q8zyy3 pyrobaculum
7	31	23.5	15	1	SODM_ENTAE	P22799 enterobacte
8	31	23.5	18	2	Q9QZX4	Q9qzx4 mus spretus
9	31	23.5	18	2	Q9QZX5	Q9qzx5 mus musculu
10	31	23.5	19	2	Q9UC80	Q9uc80 homo sapien
11	31	23.5	27	2	Q9NJT6	Q9njt6 leishmania
12	30	22.7	28	2	O65311	O65311 arabidopsis
13	29	22.0	16	2	Q7M137	Q7m137 unidentifie
14	29	22.0	19	1	OXLA_OPHHA	P81383 ophiophagus
15	29	22.0	22	2	Q7M0Z8	Q7m0z8 nocardia as
16	29	22.0	25	2	Q7PCW4	Q7pcw4 plasmodium
17	29	22.0	25	2	Q7RLH1	Q7rlh1 plasmodium
18	29	22.0	26	2	Q9CS32	Q9cs32 mus musculu
19	29	22.0	27	2	Q25867	Q25867 plasmodium
20	29	22.0	27	2	Q661K4	Q661k4 borrelia ga
21	28.5	21.6	24	2	Q9RQ27	Q9rq27 clostridium
22	28	21.2	15	2	Q6TAR1	Q6tar1 homo sapien
23	28	21.2	21	2	Q63813	Q63813 rattus sp.
24	28	21.2	22	2	Q91QR9	Q91qr9 cauliflower
25	28	21.2	23	2	Q9UWL6	Q9uwl6 methanosarc
26	28	21.2	24	2	Q9GNE5	Q9gne5 caenorhabdi
27	28	21.2	26	2	Q9UWF9	Q9uwf9 methanosarc
28	28	21.2	26	2	Q71QT7	Q71qt7 flavescence
29	28	21.2	26	2	Q99JC5	Q99jc5 rattus sp.
30	28	21.2	28	2	Q9RAT7	Q9rat7 lactococcus
31	27	20.5	15	2	Q6LDF5	Q6ldf5 trichostron
32	27	20.5	17	2	Q9PS13	Q9ps13 gallus gall
33	27	20.5	20	2	Q8S9F3	Q8s9f3 nicotiana s
34	27	20.5	21	2	Q46010	Q46010 clostridium
35	27	20.5	21	2	Q46011	Q46011 clostridium
36	27	20.5	22	2	Q6VRW6	Q6vrw6 fissidens s
37	27	20.5	24	2	Q9TR68	Q9tr68 sus scrofa
38	27	20.5	24	2	Q9KIL2	Q9kil2 streptomyce
39	27	20.5	24	2	Q9REH8	Q9reh8 borrelia bu
40	27	20.5	25	2	Q9R4S5	Q9r4s5 streptomyce
41	27	20.5	25	2	Q9R5J4	Q9r5j4 escherichia
42	27	20.5	26	2	Q9T2S3	Q9t2s3 solanum tub
43	27	20.5	26	2	Q64FW9	Q64fw9 cauliflower
44	26.5	20.1	26	1	Y126_ARCFU	O30111 archaeoglob
45	26.5	20.1	26	2	Q9BM05	Q9bm05 habrotrocha

ALIGNMENTS

RESULT 1
SODF_PASPI
ID SODF_PASPI STANDARD; PRT; 20 AA.
AC P81527;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
GN Name=sodB;
OS Pasteurella piscicida (Photobacterium damsela (subsp. piscicida)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=38294;
RN [1]
RP SEQUENCE.
RC STRAIN=MT1415;
RX MEDLINE=99173752; PubMed=10075430;
RA Barnes A.C., Balebona M.C., Horne M.T., Ellis A.E.;
RT "Superoxide dismutase and catalase in Photobacterium damselae subsp.
RT piscicida and their roles in resistance to reactive oxygen species.";
RL Microbiology 145:483-494(1999).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR HSSP; P09157; 1ISC.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; Sod_Fe_N; 1.
KW Direct protein sequencing; Iron; Metal-binding; Oxidoreductase;
KW Periplasmic.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2153 MW; A8D31FDAE8553B6D CRC64;

Query Match 28.8%; Score 38; DB 1; Length 20;
Best Local Similarity 61.5%; Pred. No. 1e+03;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy         15 EIDALEYENDALE 27
              |: || |  ||||
Db          3 ELPALPYAKDALE 15
```

RESULT 2
Q9UCS1
ID Q9UCS1 PRELIMINARY; PRT; 23 AA.
AC Q9UCS1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE TROPOMYOSIN=33 kDa calcium binding protein fragment A (Fragment).

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RA   Crabos M., Yamakado T., Heizmann C.W., Cerletti N., Buhler F.R.,
RA   Erne P.;
RT   "The calcium binding protein tropomyosin in human platelets and
RT   cardiac tissue: elevation in hypertensive cardiac hypertrophy.";
RL   Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
FT   NON_TER       1      1
FT   NON_TER      23     23
SQ   SEQUENCE   23 AA;  2475 MW;  EBD4B463017E7716 CRC64;

  Query Match             28.8%;  Score 38;  DB 2;  Length 23;
  Best Local Similarity   47.1%;  Pred. No. 1.2e+03;
  Matches    8;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 ALKQKIASLKQEIDALE 20
              |:| || :|:|: |  |
Db          1 AVKKKIQALQQQADEAE 17


RESULT 3
Q7RR69
ID   Q7RR69      PRELIMINARY;      PRT;    26 AA.
AC   Q7RR69;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein (Fragment).
GN   Name=PY00865;
OS   Plasmodium yoelii yoelii.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=73239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=17XNL;
RX   PubMed=12368865; DOI=10.1038/nature01099;
RA   Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA   Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA   Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA   Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA   Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA   Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA   Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA   van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA   Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA   Carucci D.J.;
RT   "Genome sequence and comparative analysis of the model rodent malaria
RT   parasite Plasmodium yoelii yoelii.";
RL   Nature 419:512-519(2002).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABL01000232; EAA19000.1; -.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   26 AA;  3147 MW;  C3507C4723F4490A CRC64;

  Query Match             26.5%;  Score 35;  DB 2;  Length 26;
  Best Local Similarity   35.0%;  Pred. No. 3e+03;
  Matches    7;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 ALKQKIASLKQEIDALEYEN 23
              | |:|    |:| ::| |::
Db          2 AFKRKAKKYKEENESLIYDS 21


RESULT 4
O44710
ID   O44710      PRELIMINARY;      PRT;    22 AA.
AC   O44710;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Tropomyosin 1 isoform e (Fragment).
GN   Name=Tm1;
OS   Drosophila pseudoobscura (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7237;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Goldendale 3;
RX   MEDLINE=99442389; PubMed=10511563;
RA   Hamblin M.T., Aquadro C.F.;
RT   "DNA sequence variation and the recombinational landscape in
RT   Drosophila pseudoobscura. A study of the second chromosome.";
RL   Genetics 153:859-869(1999).
DR   EMBL; AF039274; AAB96670.1; -.
DR   EMBL; AF039273; AAB96670.1; JOINED.
DR   FlyBase; FBgn0025413; Dpse\Tm1.
DR   InterPro; IPR000533; Tropomyosin.
DR   Pfam; PF00261; Tropomyosin; 1.
FT   NON_TER       1      1
FT   NON_TER      22     22
SQ   SEQUENCE   22 AA;  2611 MW;  F86B844608F4175C CRC64;

  Query Match             25.8%;  Score 34;  DB 2;  Length 22;
  Best Local Similarity   35.3%;  Pred. No. 3.3e+03;
  Matches    6;  Conservative    7;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          6 KQKIASLKQEIDALEYE 22
              ::::  |::|:| || |
Db          2 EKQVKRLQKEVDRLEDE 18


RESULT 5
Q95Y34
ID   Q95Y34      PRELIMINARY;      PRT;    16 AA.
AC   Q95Y34;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein Y108G3AL.6.
GN   Name=Y108G3AL.6; ORFNames=Y108G3AL.6;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   WormBase Consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Courtney L.;
RT   "The sequence of C. elegans cosmid Y108G3AL.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.H.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
```

```
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilson R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [11]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilson R.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [12]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RG   WormBase Consortium;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC024744; AAL13326.1; -.
DR   WormBase; WBGene00022437; Y108G3AL.6.
DR   WormPep; Y108G3AL.6; CE29605.
KW   Hypothetical protein.
SQ   SEQUENCE   16 AA;  1904 MW;  4932099B5AA361E5 CRC64;

  Query Match             24.2%;  Score 32;  DB 2;  Length 16;
  Best Local Similarity   35.7%;  Pred. No. 4.2e+03;
  Matches    5;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         15 EIDALEYENDALEQ 28
              |:|  :||:  :|:
Db          2 EVDDSDYEDSDIEE 15


RESULT 6
Q8ZYY3
ID   Q8ZYY3      PRELIMINARY;      PRT;    28 AA.
AC   Q8ZYY3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein PAE0551.
GN   OrderedLocusNames=PAE0551;
OS   Pyrobaculum aerophilum.
OC   Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC   Thermoproteaceae; Pyrobaculum.
OX   NCBI_TaxID=13773;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IM2;
RX   MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA   Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA   Miller J.H.;
RT   "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT   aerophilum.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR   EMBL; AE009773; AAL62858.1; -.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   28 AA;  3001 MW;  869F81422C53A14D CRC64;

  Query Match             24.2%;  Score 32;  DB 2;  Length 28;
  Best Local Similarity   33.3%;  Pred. No. 7.2e+03;
  Matches    6;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          2 IAALKQKIASLKQEIDAL 19
              :| :|  :| ||  : :|
Db          3 VAEIKASVAELKVAVGSL 20


RESULT 7
SODM_ENTAE
ID   SODM_ENTAE     STANDARD;      PRT;    15 AA.
AC   P22799;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
GN   Name=sodA;
OS   Enterobacter aerogenes (Aerobacter aerogenes).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Enterobacter.
OX   NCBI_TaxID=548;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=91248479; PubMed=1368658;
RA   Kim S.W., Lee S.O., Lee T.H.;
RT   "Purification and characterization of superoxide dismutase from
RT   Aerobacter aerogenes.";
RL   Agric. Biol. Chem. 55:101-108(1991).
CC   -!- FUNCTION: Destroys radicals which are normally produced within the
CC       cells and which are toxic to biological systems.
CC   -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC   -!- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC   -!- SUBUNIT: Homodimer.
CC   -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC       family.
DR   PIR; PN0615; PN0615.
DR   InterPro; IPR001189; SODismutase.
DR   Pfam; PF00081; Sod_Fe_N; 1.
DR   PROSITE; PS00088; SOD_MN; PARTIAL.
KW   Direct protein sequencing; Iron; Metal-binding; Oxidoreductase.
FT   NON_TER      15      15
SQ   SEQUENCE   15 AA;  1756 MW;  352F3D949202E642 CRC64;

  Query Match             23.5%;  Score 31;  DB 1;  Length 15;
  Best Local Similarity   53.8%;  Pred. No. 5.2e+03;
  Matches    7;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         15 EIDALEYENDALE 27
              |:  | |  ||||
Db          3 ELPQLPYAYDALE 15


RESULT 8
Q9QZX4
ID   Q9QZX4      PRELIMINARY;      PRT;    18 AA.
AC   Q9QZX4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Desmoplakin (Fragment).
GN   Name=Dsp;
OS   Mus spretus (Western wild mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10096;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Green K.J., Guy S.G., Cserhalmi-Friedman P., McLean W.H.I.,
RA   Christiano A.M., Wagner R.M.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF148515; AAF02528.1; -.
DR   MGD; MGI:109611; Dsp.
FT   NON_TER       1      1
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  2289 MW;  3B41DF23C1E2F960 CRC64;

  Query Match           23.5%;  Score 31;  DB 2;  Length 18;
  Best Local Similarity   41.2%;  Pred. No. 6.2e+03;
  Matches    7;  Conservative    6;  Mismatches    2;  Indels    2;  Gaps    1;

Qy         11 SLKQEIDALEYENDALE 27
              :|:|||:  :::  |||
Db          4 NLRQEIE--KFQKQALE 18


RESULT 9
Q9QZX5
ID   Q9QZX5      PRELIMINARY;      PRT;    18 AA.
AC   Q9QZX5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Desmoplakin (Fragment).
GN   Name=Dsp;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C75BL6/J;
RA   Green K.J., Guy S.G., Cserhalmi-Friedman P., McLean W.H.I.,
RA   Christiano A.M., Wagner R.M.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF148514; AAF02527.1; -.
DR   MGD; MGI:109611; Dsp.
DR   GO; GO:0016323; C:basolateral plasma membrane; IDA.
DR   GO; GO:0030057; C:desmosome; IDA.
DR   GO; GO:0005739; C:mitochondrion; IDA.
FT   NON_TER       1      1
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  2289 MW;  3B41DF23C1E2F960 CRC64;

  Query Match           23.5%;  Score 31;  DB 2;  Length 18;
  Best Local Similarity   41.2%;  Pred. No. 6.2e+03;
  Matches    7;  Conservative    6;  Mismatches    2;  Indels    2;  Gaps    1;

Qy         11 SLKQEIDALEYENDALE 27
              :|:|||:  :::  |||
Db          4 NLRQEIE--KFQKQALE 18


RESULT 10
Q9UC80
ID   Q9UC80      PRELIMINARY;      PRT;    19 AA.
AC   Q9UC80;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   21.5 kDa stone matrix protein (EC 1.15.1.1) (Superoxide dismutase
DE   [Mn/Fe]) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RA   Binette J.P., Binette M.B.;
RT   "Sequencing of proteins extracted from stones.";
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Destroys radicals which are normally produced within the
CC       cells and which are toxic to biological systems (By similarity).
CC   -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC   -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC       family.
DR   HSSP; P09223; 1DT0.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR   GO; GO:0006801; P:superoxide metabolism; IEA.
DR   InterPro; IPR001189; SODismutase.
DR   Pfam; PF00081; Sod_Fe_N; 1.
KW   Oxidoreductase.
SQ   SEQUENCE   19 AA;  2116 MW;  A0D0DAE848EE7894 CRC64;

  Query Match           23.5%;  Score 31;  DB 2;  Length 19;
  Best Local Similarity   46.2%;  Pred. No. 6.5e+03;
  Matches    6;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         15 EIDALEYENDALE 27
              |:  | | :|||:
Db          3 ELPPLPYAHDALQ 15


RESULT 11
Q9NJT6
ID   Q9NJT6      PRELIMINARY;      PRT;    27 AA.
AC   Q9NJT6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Major paraflagellar rod protein (Fragment).
OS   Leishmania major.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=5664;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ch'ang L.Y., Lee T.;
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF110672; AAF66093.1; -.
DR   GO; GO:0019861; C:flagellum; IEA.
KW   Flagellum.
FT   NON_TER       1      1
FT   NON_TER      27     27
SQ   SEQUENCE   27 AA;  3005 MW;  0C5ADB2B6B425ED9 CRC64;

  Query Match           23.5%;  Score 31;  DB 2;  Length 27;
  Best Local Similarity   53.8%;  Pred. No. 9.1e+03;
  Matches    7;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IAALKQKIASLKQ 14
              | |||: :  |||
Db          1 IVALKKTLNELKQ 13


RESULT 12
O65311
ID   O65311      PRELIMINARY;      PRT;    28 AA.
AC   O65311;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Beta-9 tubulin (Fragment).
GN   Name=TUB9;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sanders P.M., Bui A.Q., Weterings K., McIntire K.N., Hsu Y.C.,
RA   Lee P.Y., Truong M.T., Beals T.B., Goldberg R.B.;
RT   "Anther Development Defects in Arabidopsis thaliana Male-Sterile
RT   Mutants.";
RL   Sex. Plant Reprod. 11:297-322(1999).
DR   EMBL; AF060248; AAC97107.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   28 AA;  3388 MW;  8060E4E537BE670E CRC64;

  Query Match             22.7%;  Score 30;  DB 2;  Length 28;
  Best Local Similarity   37.5%;  Pred. No. 1.2e+04;
  Matches    9;  Conservative    3;  Mismatches    8;  Indels    4;  Gaps    1;

Qy          9 IASLKQEIDAL----EYENDALEQ 28
              :|  :|  ||     |||  |  |:
Db          3 VAEYQQYQDATVGEEEYEEDEEEE 26


RESULT 13
Q7M137
ID   Q7M137      PRELIMINARY;      PRT;    16 AA.
AC   Q7M137;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Superoxide dismutase (EC 1.15.1.1) (Fragment).
OS   unidentified bacterium.
OC   Bacteria; environmental samples.
OX   NCBI_TaxID=2338;
RN   [1]
RP   SEQUENCE.
RA   Binette J.P., Binette M.B.;
RL   Submitted (OCT-1996) to the PIR data bank.
CC   -!- FUNCTION: Destroys radicals which are normally produced within the
CC       cells and which are toxic to biological systems (By similarity).
CC   -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC   -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC       family.
DR   PIR; E58503; E58503.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR   GO; GO:0006801; P:superoxide metabolism; IEA.
DR   InterPro; IPR001189; SODismutase.
DR   Pfam; PF00081; Sod_Fe_N; 1.
KW   Oxidoreductase.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1828 MW;  12DE78949AC43609 CRC64;

  Query Match             22.0%;  Score 29;  DB 2;  Length 16;
  Best Local Similarity   40.0%;  Pred. No. 9.5e+03;
  Matches    6;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         12 LKQEIDALEYENDAL 26
              ::  :  | || |||
Db          1 MEHTLPPLPYEMDAL 15


RESULT 14
OXLA_OPHHA
ID   OXLA_OPHHA     STANDARD;      PRT;    19 AA.
AC   P81383;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   L-amino-acid oxidase (EC 1.4.3.2) (LAO) (LAAO) (Fragment).
OS   Ophiophagus hannah (King cobra) (Naja hannah).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Elapidae; Elapinae; Ophiophagus.
OX   NCBI_TaxID=8665;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=94361525; PubMed=8080286; DOI=10.1006/abbi.1994.1401;
RA   Ponnudurai G., Chung M.C.M., Tan N.-H.;
RT   "Purification and properties of the L-amino acid oxidase from Malayan
RT   pit viper (Calloselasma rhodostoma) venom.";
RL   Arch. Biochem. Biophys. 313:373-378(1994).
RN   [2]
RP   SEQUENCE OF 1-15.
RC   TISSUE=Venom;
RX   MEDLINE=97449790; PubMed=9304806; DOI=10.1016/S1357-2725(97)00024-1;
RA   Ahn M.Y., Lee B.M., Kim Y.S.;
RT   "Characterization and cytotoxicity of L-amino acid oxidase from the
RT   venom of king cobra (Ophiophagus hannah).";
RL   Int. J. Biochem. Cell Biol. 29:911-919(1997).
CC   -!- FUNCTION: Has cytotoxic activity (By similarity).
CC   -!- CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid
CC       + NH(3) + H(2)O(2).
CC   -!- COFACTOR: FAD.
CC   -!- SUBUNIT: Homodimer (Probable).
CC   -!- PTM: Glycosylated.
CC   -!- SIMILARITY: Belongs to the flavin monoamine oxidase family.
CC       Strong, to mammalian FIG1.
KW   Direct protein sequencing; FAD; Flavoprotein; Glycoprotein;
KW   Oxidoreductase; Toxin.
FT   CONFLICT      1      1       H -> S (in Ref. 2).
FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  2298 MW;  DD911A5B414F1427 CRC64;

  Query Match             22.0%;  Score 29;  DB 1;  Length 19;
  Best Local Similarity   33.3%;  Pred. No. 1.1e+04;
  Matches    5;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          9 IASLKQEIDALEYEN 23
              : :|::     ||||
Db          2 VINLEESFQEPEYEN 16


RESULT 15
Q7M0Z8
ID   Q7M0Z8      PRELIMINARY;      PRT;    22 AA.
AC   Q7M0Z8;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Ribosomal protein L30 (Fragment).
OS   Nocardia asteroides.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Nocardiaceae; Nocardia.
OX   NCBI_TaxID=1824;
RN   [1]
RP   SEQUENCE.
RA   Ochi K.;
RL   Submitted (FEB-1994) to the PIR data bank.
DR   PIR; JP0066; JP0066.
FT   NON_TER       1      1
FT   NON_TER      22     22
SQ   SEQUENCE   22 AA;  2330 MW;  5C7E71FB6FD577CA CRC64;

  Query Match             22.0%;  Score 29;  DB 2;  Length 22;
  Best Local Similarity   31.6%;  Pred. No. 1.3e+04;
  Matches    6;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          8 KIASLKQEIDALEYENDAL 26
              |:  :|  | |   : |:|
Db          4 KVTQIKSTIGAKANQKDSL 22


Search completed: April 27, 2005, 15:06:16
Job time : 122 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2005, 14:45:41 ; Search time 122 Seconds
(without alignments)
88.765 Million cell updates/sec

Title: US-10-088-417A-4
Perfect score: 137
Sequence: 1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 794064

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	137	100.0	28	4	AAB74346	Aab74346 Peptide S
2	137	100.0	28	4	AAB74347	Aab74347 Peptide S
3	124	90.5	28	4	AAB74349	Aab74349 Peptide S
4	123	89.8	28	4	AAB74348	Aab74348 Peptide S
5	123	89.8	28	4	AAB74356	Aab74356 Peptide u
6	123	89.8	28	4	AAB74352	Aab74352 Peptide S
7	122	89.1	28	4	AAB74345	Aab74345 Peptide S
8	105	76.6	28	8	ADM41438	Adm41438 Self-asse
9	100	73.0	27	8	ADM41437	Adm41437 Self-asse
10	81	59.1	28	7	ABR84737	Abr84737 DE novo d
11	75	54.7	28	4	AAB74343	Aab74343 Peptide S
12	75	54.7	28	4	AAB74351	Aab74351 Peptide S
13	75	54.7	28	8	ADM41436	Adm41436 Self-asse
14	74	54.0	28	4	AAB74341	Aab74341 Peptide S
15	74	54.0	28	4	AAB74342	Aab74342 Peptide S
16	70	51.1	28	4	AAB74355	Aab74355 Peptide u
17	70	51.1	28	4	AAB74350	Aab74350 Peptide S
18	68	49.6	25	3	AAB08382	Aab08382 Peptide u
19	59	43.1	28	7	ABR84735	Abr84735 DE novo d
20	55	40.1	18	4	AAB74340	Aab74340 Peptide C
21	55	40.1	25	3	AAB08381	Aab08381 Peptide u
22	54	39.4	28	7	ABR84736	Abr84736 DE novo d
23	51	37.2	24	3	AAB21683	Aab21683 Colied co
24	51	37.2	24	7	ADD93917	Add93917 Coiled co
25	50	36.5	23	3	AAB08388	Aab08388 Peptide u
26	50	36.5	23	6	ADA00699	Ada00699 Protein m
27	47	34.3	14	2	AAW71411	Aaw71411 Peptide f
28	47	34.3	14	2	AAW80528	Aaw80528 Beta-shee
29	47	34.3	15	2	AAW71417	Aaw71417 Peptide f
30	47	34.3	15	2	AAW80545	Aaw80545 Peptide h
31	47	34.3	17	2	AAW71423	Aaw71423 Peptide h
32	47	34.3	21	5	ABG78944	Abg78944 Human bre
33	47	34.3	21	6	ABJ37799	Abj37799 Human tum
34	47	34.3	21	6	ABJ37767	Abj37767 Human tum
35	47	34.3	21	7	ADL93196	Adl93196 Human bre
36	47	34.3	21	7	ADL93249	Adl93249 Human bre
37	46	33.6	17	4	AAB74344	Aab74344 Peptide C
38	45	32.8	28	4	AAU14021	Aau14021 Peptide s
39	45	32.8	28	6	ABO10240	Abo10240 Heptad re
40	45	32.8	28	7	ADB67071	Adb67071 Canonical
41	45	32.8	28	8	ADL99341	Adl99341 Nanostruc
42	44	32.1	24	3	AAY95963	Aay95963 Coiled-co
43	44	32.1	28	2	AAR31979	Aar31979 SSP4 poly
44	43	31.4	14	7	ADI39146	Adi39146 Amphipath
45	43	31.4	20	6	ABJ37808	Abj37808 Human tum

ALIGNMENTS

RESULT 1
AAB74346
ID AAB74346 standard; peptide; 28 AA.
XX
AC AAB74346;
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p2B.
XX
KW Atomic Force Microscopy; AFM.
XX
OS Unidentified.
XX
PN WO200121646-A1.
XX
PD 29-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-GB003576.
XX
PR 17-SEP-1999; 99GB-00022013.
XX
PA (UYSU-) UNIV SUSSEX.
XX
PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX
DR WPI; 2001-335468/35.
XX
PT New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
PS Disclosure; Page 9; 45pp; English.
XX
CC The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p2B
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 137; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
||||||||||||||||||||||||||||

```
Db          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28


RESULT 2
AAB74347
ID   AAB74347 standard; peptide; 28 AA.
XX
AC   AAB74347;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p2C.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Claim 16; Page 26; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is the peptide monomer unit SAF-p2C
XX
SQ   Sequence 28 AA;

  Query Match             100.0%;  Score 137;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-11;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
              ||||||||||||||||||||||||||||
Db          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28


RESULT 3
AAB74349
ID   AAB74349 standard; peptide; 28 AA.
XX
AC   AAB74349;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p2E.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Disclosure; Page 9; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is the peptide monomer unit SAF-p2E
XX
SQ   Sequence 28 AA;

  Query Match             90.5%;  Score 124;  DB 4;  Length 28;
  Best Local Similarity   96.4%;  Pred. No. 1.7e-09;
  Matches   27;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
              |||||| ||||||||||||||||||||||
Db          1 KIRALKCKNAHLKQEIAALEQEIAALEQ 28


RESULT 4
AAB74348
ID   AAB74348 standard; peptide; 28 AA.
XX
AC   AAB74348;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p2D.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Disclosure; Page 9; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is the peptide monomer unit SAF-p2D
XX
SQ   Sequence 28 AA;
```

```
  Query Match             89.8%;  Score 123;  DB 4;  Length 28;
  Best Local Similarity   96.4%;  Pred. No. 2.4e-09;
  Matches   27;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
              |||||| ||||||||||||||||||||||
Db          1 KIRALKAKNAHLKQEIAALEQEIAALEQ 28


RESULT 5
AAB74356
ID   AAB74356 standard; peptide; 28 AA.
XX
AC   AAB74356;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide used to form blunt-ended heterodimers.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Disclosure; Fig 8; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is a peptide used to form blunt-ended heterodimers
XX
SQ   Sequence 28 AA;

  Query Match             89.8%;  Score 123;  DB 4;  Length 28;
  Best Local Similarity   96.4%;  Pred. No. 2.4e-09;
  Matches   27;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
              |||||| ||||||||||||||||||||||
Db          1 KIRALKAKNAHLKQEIAALEQEIAALEQ 28


RESULT 6
AAB74352
ID   AAB74352 standard; peptide; 28 AA.
XX
AC   AAB74352;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p2.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Claim 16; Page 26; 45pp; English.
XX
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is the peptide monomer unit SAF-p2
XX
SQ   Sequence 28 AA;

  Query Match             89.8%;  Score 123;  DB 4;  Length 28;
  Best Local Similarity   96.4%;  Pred. No. 2.4e-09;
  Matches   27;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
              |||||| ||||||||||||||||||||||
Db          1 KIRALKAKNAHLKQEIAALEQEIAALEQ 28


RESULT 7
AAB74345
ID   AAB74345 standard; peptide; 28 AA.
XX
AC   AAB74345;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Peptide SAF-p2A.
XX
KW   Atomic Force Microscopy; AFM.
XX
OS   Unidentified.
XX
PN   WO200121646-A1.
XX
PD   29-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-GB003576.
XX
PR   17-SEP-1999;   99GB-00022013.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson DN,  Walshaw J,  Pandya MJ,  Colyer J;
XX
DR   WPI; 2001-335468/35.
XX
PT   New protein structures with peptide monomer units, useful in Atomic Force
PT   Microscopy, purifying biological fluids, promoting tissue repair and
PT   tissue engineering, or constructing nanoscale molecular sieves.
XX
PS   Disclosure; Page 9; 45pp; English.
XX
```

```
CC   The present invention relates to a protein structure with several first
CC   peptide monomer units arranged in a first strand and several second
CC   peptide monomer units arranged in a second strand. The structure is
CC   useful in Atomic Force Microscopy and a number of other applications. The
CC   present sequence is the peptide monomer unit SAF-p2A
XX
SQ   Sequence 28 AA;

  Query Match             89.1%;  Score 122;  DB 4;  Length 28;
  Best Local Similarity   92.9%;  Pred. No. 3.2e-09;
  Matches   26;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
              || ||||||| ||||||||||||||||||
Db          1 KISALKWKNASLKQEIAALEQEIAALEQ 28


RESULT 8
ADM41438
ID   ADM41438 standard; peptide; 28 AA.
XX
AC   ADM41438;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Self-assembling peptide fibre SAF-p2a.
XX
KW   Fibre-shaping peptide; self-assembling peptide.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal NH3 moiety"
XX
PN   WO2004022584-A1.
XX
PD   18-MAR-2004.
XX
PF   08-SEP-2003; 2003WO-GB003900.
XX
PR   06-SEP-2002; 2002GB-00020805.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson D,  Ryadnov MG;
XX
DR   WPI; 2004-248444/23.
XX
PT   Novel fiber-shaping peptide comprising hub and several peptide monomer
PT   units, useful for producing protein structure useful in purification of
PT   biological fluids and in surface engineering procedures.
XX
PS   Example 36; Page 22; 37pp; English.
XX
CC   The present sequence is that of self-assembling peptide fibre (SAF) SAF-
CC   p2a. The invention relates to fibre-shaping (FiSh) peptides ADM41434-
CC   ADM41435 that are capable of interacting with SAFs to form protein
CC   structures. The FiSh peptides allow morphological changes (branches,
CC   splits, kinks and bends) to be made to protein fibres comprising SAFs. By
CC   incorporating such morphological changes in the protein fibres, it is
CC   possible to generate a variety of (nanoscale) protein structures, such as
CC   assemblies in general, including matrix, filter, network, grid and
CC   scaffold structures. Use of the protein structures in the purification of
CC   biological fluids, for assembling cells for cell and tissue engineering,
CC   and in surface engineering procedures is claimed.
XX
SQ   Sequence 28 AA;

  Query Match             76.6%;  Score 105;  DB 8;  Length 28;
  Best Local Similarity   85.7%;  Pred. No. 5.9e-07;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
              ||| || ||| |||||||||| |||||||
Db          1 KIRRLKQKNARLKQEIAALEYEIAALEQ 28


RESULT 9
ADM41437
ID   ADM41437 standard; peptide; 27 AA.
XX
AC   ADM41437;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Self-assembling peptide fibre (SAF).
XX
KW   Fibre-shaping peptide; self-assembling peptide.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal NH3 moiety"
XX
PN   WO2004022584-A1.
XX
PD   18-MAR-2004.
XX
PF   08-SEP-2003; 2003WO-GB003900.
XX
PR   06-SEP-2002; 2002GB-00020805.
XX
PA   (UYSU-) UNIV SUSSEX.
XX
PI   Woolfson D,  Ryadnov MG;
XX
DR   WPI; 2004-248444/23.
XX
PT   Novel fiber-shaping peptide comprising hub and several peptide monomer
PT   units, useful for producing protein structure useful in purification of
PT   biological fluids and in surface engineering procedures.
XX
PS   Example 30; Page 22; 37pp; English.
XX
CC   The present sequence is that of a self-assembling peptide fibre (SAF).
CC   The invention relates to fibre-shaping (FiSh) peptides ADM41434-ADM41435
CC   that are capable of interacting with SAFs to form protein structures. The
CC   FiSh peptides allow morphological changes (branches, splits, kinks and
CC   bends) to be made to protein fibres comprising SAFs. By incorporating
CC   such morphological changes in the protein fibres, it is possible to
CC   generate a variety of (nanoscale) protein structures, such as assemblies
CC   in general, including matrix, filter, network, grid and scaffold
CC   structures. Use of the protein structures in the purification of
CC   biological fluids, for assembling cells for cell and tissue engineering,
CC   and in surface engineering procedures is claimed.
XX
SQ   Sequence 27 AA;

  Query Match             73.0%;  Score 100;  DB 8;  Length 27;
  Best Local Similarity   85.2%;  Pred. No. 2.7e-06;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IRALKWKNAHLKQEIAALEQEIAALEQ 28
              || || ||| |||||||||| |||||||
Db          1 IRRLKQKNARLKQEIAALEYEIAALEQ 27


RESULT 10
ABR84737
ID   ABR84737 standard; peptide; 28 AA.
XX
AC   ABR84737;
XX
DT   18-DEC-2003  (first entry)
```

XX
DE DE novo designed AHEC peptide #5.
XX
KW Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
KW AHEC; antiparallel; drug targeting.
XX
OS Synthetic.
XX
PN WO2003066660-A2.
XX
PD 14-AUG-2003.
XX
PF 05-FEB-2003; 2003WO-EP001217.
XX
PR 05-FEB-2002; 2002US-0354376P.
XX
PA (IMMU-) IMMUNOLEX THERAPEUTICS APS.
XX
PI Caterer NR, Uttental LO, Neilson RW;
XX
DR WPI; 2003-679535/64.
XX
PT Composition useful for forming therapeutic antibodies and antibody
PT fragments comprises pair of antibody Fv fragments linked and stabilized
PT by antiparallel heterogeneous alpha-helical coiled-coil peptides.
XX
PS Disclosure; Page 14; 35pp; English.
XX
CC The present invention relates to a composition which comprises a pair of
CC antibody Fv fragments linked and stabilised by antiparallel heterogeneous
CC alpha-helical coiled-coil (AHEC) peptides. The composition is used to
CC form multimeric complexes and therapeutic antibodies and antibody
CC fragments useful for e.g. inhibition of receptor binding and the
CC targeting of drugs, toxins and labels in research, industry and
CC healthcare. The present sequence is an AHEC peptide used in the
CC exemplification of the invention
XX
SQ Sequence 28 AA;

Query Match 59.1%; Score 81; DB 7; Length 28;
Best Local Similarity 64.0%; Pred. No. 0.00095;
Matches 16; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 4 ALKWKNAHLKQEIAALEQEIAALEQ 28
Db 1 AIKYKQAAIKNEIAAIKQEIAAIEQ 25

RESULT 11
AAB74343
ID AAB74343 standard; peptide; 28 AA.
XX
AC AAB74343;
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p1C.
XX
KW Atomic Force Microscopy; AFM.
XX
OS Unidentified.
XX
PN WO200121646-A1.
XX
PD 29-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-GB003576.
XX
PR 17-SEP-1999; 99GB-00022013.
XX
PA (UYSU-) UNIV SUSSEX.
XX
PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX
DR WPI; 2001-335468/35.
XX
PT New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
PS Claim 16; Page 26; 45pp; English.
XX
CC The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p1C
XX
SQ Sequence 28 AA;

Query Match 54.7%; Score 75; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.006;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
Db 1 KIAALKQKIASLKQEIDALEYENDALEQ 28

RESULT 12
AAB74351
ID AAB74351 standard; peptide; 28 AA.
XX
AC AAB74351;
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p1.
XX
KW Atomic Force Microscopy; AFM.
XX
OS Unidentified.
XX
PN WO200121646-A1.
XX
PD 29-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-GB003576.
XX
PR 17-SEP-1999; 99GB-00022013.
XX
PA (UYSU-) UNIV SUSSEX.
XX
PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX
DR WPI; 2001-335468/35.
XX
PT New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
PS Claim 16; Page 26; 45pp; English.
XX
CC The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p1
XX
SQ Sequence 28 AA;

Query Match 54.7%; Score 75; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.006;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28

```
                    || ||| | | ||||| ||| |  ||||
Db          1 KIAALKQKIASLKQEIDALEYENDALEQ 28
```

RESULT 13
ADM41436
ID ADM41436 standard; peptide; 28 AA.
XX
AC ADM41436;
XX
DT 03-JUN-2004 (first entry)
XX
DE Self-assembling peptide fibre SAF-p1.
XX
KW Fibre-shaping peptide; self-assembling peptide.
XX
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT Modified-site   1
FT   /note= "N-terminal NH3 moiety"
XX
PN WO2004022584-A1.
XX
PD 18-MAR-2004.
XX
PF 08-SEP-2003; 2003WO-GB003900.
XX
PR 06-SEP-2002; 2002GB-00020805.
XX
PA (UYSU-) UNIV SUSSEX.
XX
PI Woolfson D, Ryadnov MG;
XX
DR WPI; 2004-248444/23.
XX
PT Novel fiber-shaping peptide comprising hub and several peptide monomer
PT units, useful for producing protein structure useful in purification of
PT biological fluids and in surface engineering procedures.
XX
PS Example 30; Page 22; 37pp; English.
XX
CC The present sequence is that of self-assembling peptide fibre (SAF) SAF-
CC p1. The invention relates to fibre-shaping (FiSh) peptides ADM41434-
CC ADM41435 that are capable of interacting with SAFs to form protein
CC structures. The FiSh peptides allow morphological changes (branches,
CC splits, kinks and bends) to be made to protein fibres comprising SAFs. By
CC incorporating such morphological changes in the protein fibres, it is
CC possible to generate a variety of (nanoscale) protein structures, such as
CC assemblies in general, including matrix, filter, network, grid and
CC scaffold structures. Use of the protein structures in the purification of
CC biological fluids, for assembling cells for cell and tissue engineering,
CC and in surface engineering procedures is claimed.
XX
SQ Sequence 28 AA;

```
  Query Match             54.7%;  Score 75;  DB 8;  Length 28;
  Best Local Similarity   71.4%;  Pred. No. 0.006;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
              || ||| | | ||||| ||| |  ||||
Db          1 KIAALKQKIASLKQEIDALEYENDALEQ 28
```

RESULT 14
AAB74341
ID AAB74341 standard; peptide; 28 AA.
XX
AC AAB74341;
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p1A.
XX
KW Atomic Force Microscopy; AFM.
XX
OS Unidentified.
XX
PN WO200121646-A1.
XX
PD 29-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-GB003576.
XX
PR 17-SEP-1999; 99GB-00022013.
XX
PA (UYSU-) UNIV SUSSEX.
XX
PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX
DR WPI; 2001-335468/35.
XX
PT New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
PS Claim 16; Page 26; 45pp; English.
XX
CC The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p1A
XX
SQ Sequence 28 AA;

```
  Query Match             54.0%;  Score 74;  DB 4;  Length 28;
  Best Local Similarity   71.4%;  Pred. No. 0.0082;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
              || ||| | | ||||| ||| |  ||||
Db          1 KIAALKQKIAALKQEIDALEYENDALEQ 28
```

RESULT 15
AAB74342
ID AAB74342 standard; peptide; 28 AA.
XX
AC AAB74342;
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p1B.
XX
KW Atomic Force Microscopy; AFM.
XX
OS Unidentified.
XX
PN WO200121646-A1.
XX
PD 29-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-GB003576.
XX
PR 17-SEP-1999; 99GB-00022013.
XX
PA (UYSU-) UNIV SUSSEX.
XX
PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX
DR WPI; 2001-335468/35.
XX
PT New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and

PT tissue engineering, or constructing nanoscale molecular sieves.
XX
PS Disclosure; Page 9; 45pp; English.
XX
CC The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p1B
XX
SQ Sequence 28 AA;

Query Match 54.0%; Score 74; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.0082;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy          1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
              || ||| | | ||||| ||| |  ||||
Db          1 KIAALKQKIAALKQEIDALEYENDALEQ 28
```

Search completed: April 27, 2005, 15:02:16
Job time : 123 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2005, 14:54:59 ; Search time 23.5 Seconds
(without alignments)
114.641 Million cell updates/sec

Title: US-10-088-417A-4
Perfect score: 137
Sequence: 1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 5694

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	26.3	25	2	S39391	calpain II heavy c
2	32	23.4	23	2	S23518	stromelysin (EC 3.
3	31	22.6	16	2	E37290	homeotic protein G
4	31	22.6	21	2	I65270	collagen alpha 1(I
5	30	21.9	22	2	B35372	unidentified low M
6	29	21.2	24	2	A33262	heparin-binding gr
7	29	21.2	24	2	I38253	T-cell acute lymph
8	28.5	20.8	20	2	A53592	H+-exporting ATPas
9	28	20.4	19	2	S00495	hemocyanin chain I
10	28	20.4	24	2	C47689	flagellar core pro
11	28	20.4	27	2	G61002	transformation-sen
12	27	19.7	21	2	A59325	probable bacteriop
13	26.5	19.3	27	2	PQ0844	DNA-binding protei
14	26	19.0	15	2	PA0036	glycine cleavage s
15	26	19.0	19	2	PN0467	nitrogenase (EC 1.
16	26	19.0	20	2	B46236	transforming prote
17	26	19.0	25	2	B47689	flagellar core pro
18	25	18.2	10	2	A43405	6-phosphofructo-2-
19	25	18.2	20	2	S35970	ribosomal protein
20	25	18.2	21	2	S35978	ribosomal protein
21	25	18.2	23	2	S35975	ribosomal protein
22	25	18.2	23	2	S35976	ribosomal protein
23	25	18.2	24	2	I46513	troponin I - rabbi
24	25	18.2	25	1	JC4278	ribosomal protein
25	25	18.2	25	2	JQ1617	ribosomal protein
26	25	18.2	25	2	JC4685	ribosomal protein
27	25	18.2	25	2	S38425	ribosomal protein
28	25	18.2	25	2	T49214	ribosomal protein
29	25	18.2	25	2	T06233	ribosomal protein
30	25	18.2	26	2	A37476	hypothetical prote
31	25	18.2	27	2	B33420	globin II - polych
32	24.5	17.9	26	2	C61590	beta-lactoglobulin
33	24.5	17.9	26	4	T07533	probable photosyst
34	24	17.5	17	2	PC2319	proteasome endopep
35	24	17.5	19	2	S20274	quinoline oxidored
36	24	17.5	19	2	A44854	L-2,4-diaminobutyr
37	24	17.5	20	2	PC1240	calcium-binding pr
38	24	17.5	20	2	S74101	alkaline phosphata
39	24	17.5	24	2	T46628	hypothetical prote
40	24	17.5	24	2	S33302	hydrogenase (EC 1.
41	24	17.5	25	2	B34461	heat shock protein
42	24	17.5	26	2	B55244	tubulin alpha-2 ch
43	24	17.5	26	2	A55244	tubulin alpha-1 ch
44	24	17.5	26	2	S66409	long-chain-fatty-a
45	23	16.8	13	2	A86126	hypothetical prote

ALIGNMENTS

RESULT 1
S39391
calpain II heavy chain - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 08-Jun-1994 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S39391
R;Crawford, C.; Brown, N.R.; Willis, A.C.
Biochem. J. 296, 135-142, 1993
A;Title: Studies of the active site of m-calpain and the interaction with calpastatin.
A;Reference number: S39391; MUID:94071815; PMID:8250833
A;Accession: S39391
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-25 <CRA>
A;Cross-references: UNIPROT:Q7M386

Query Match 26.3%; Score 36; DB 2; Length 25;
Best Local Similarity 33.3%; Pred. No. 1.6e+02;
Matches 7; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

```
Qy          3 RALKWKNAHLKQEIAALEQEI 23
              ||:|: |:  | :   :: ||
Db          4 RAVKYLNSEKKADYQVVDDEI 24
```

RESULT 2
S23518
stromelysin (EC 3.4.24.-) - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C;Accession: S23518
R;Bayne, E.K.; Hutchinson, N.I.; Walakovits, L.A.; Donatelli, S.; Macnaul, K.L.; Harper,
Matrix 12, 173-184, 1992
A;Title: Production, purification and characterization of canine prostromelysin.
A;Reference number: S23518; MUID:93024088; PMID:1406451
A;Accession: S23518
A;Molecule type: protein
A;Residues: 1-23 <BAY>
A;Cross-references: UNIPROT:Q9TSC5
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;1-20/Domain: matrix metalloproteinase homology (fragment) <MMP>

Query Match 23.4%; Score 32; DB 2; Length 23;
Best Local Similarity 45.5%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy          6 KWKNAHLKQEI 16
              ||:  ||   |
Db          8 KWRKXHLTYRI 18
```

```
RESULT 3
E37290
homeotic protein Gsh-5 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 16-Aug-2004
C;Accession: E37290; E38809
R;Singh, G.; Kaur, S.; Stock, J.L.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Potter
Proc. Natl. Acad. Sci. U.S.A. 88, 10706-10710, 1991
A;Title: Identification of 10 murine homeobox genes.
A;Reference number: A37290; MUID:92073356; PMID:1683707
A;Accession: E37290
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-16 <SIN>
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;1-14/Domain: homeobox homology (fragment) <HOX>

  Query Match             22.6%;  Score 31;  DB 2;  Length 16;
  Best Local Similarity   50.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RALKWKNA 10
              | :||:|:
Db          8 RRMKWRNS 15


RESULT 4
I65270
collagen alpha 1(I) chain - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I65270
R;Genovese, C.; Rowe, D.; Kream, B.
Biochemistry 23, 6210-6216, 1984
A;Title: Construction of DNA sequences complementary to rat alpha-1 and alpha-2 collagen
A;Reference number: I52392; MUID:85122694; PMID:6395893
A;Accession: I65270
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-21 <RES>
A;Cross-references: UNIPROT:Q63076; GB:M12200; NID:g203191; PIDN:AAA40835.1; PID:g203195
C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology

  Query Match             22.6%;  Score 31;  DB 2;  Length 21;
  Best Local Similarity   50.0%;  Pred. No. 6.1e+02;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         11 HLKQEIAALEQE 22
              | |  || |::|
Db          8 HCKNSIAYLDEE 19


RESULT 5
B35372
unidentified low M-r protein - Yersinia pseudotuberculosis (fragment)
C;Species: Yersinia pseudotuberculosis
C;Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 09-Jul-2004
C;Accession: B35372
R;Han, O.; Miller, V.P.; Liu, H.
J. Biol. Chem. 265, 8033-8041, 1990
A;Title: Mechanistic studies of the biosynthesis of 3,6-dideoxyhexoses in Yersinia pseud
H:dichlorophenolindolphenol oxidoreductase activity.
A;Reference number: A35372; MUID:90243678; PMID:2159466
A;Accession: B35372
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <HAN>
A;Cross-references: UNIPROT:Q7M0N2

  Query Match             21.9%;  Score 30;  DB 2;  Length 22;
  Best Local Similarity   70.0%;  Pred. No. 8.7e+02;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         17 AALEQEIAAL 26
              ||| :|:|||
Db          6 AALVKELAAL 15


RESULT 6
A33262
heparin-binding growth factor A light chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Feb-1990 #sequence_revision 21-Feb-1990 #text_change 09-Jul-2004
C;Accession: A33262
R;Zarnegar, R.; Muga, S.; Enghild, J.; Michalopoulos, G.
Biochem. Biophys. Res. Commun. 163, 1370-1376, 1989
A;Title: NH-2-terminal amino acid sequence of rabbit hepatopoietin A, a heparin-binding
A;Reference number: A33262; MUID:89392048; PMID:2528955
A;Accession: A33262
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-24 <ZAR>
A;Cross-references: UNIPROT:P13571
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: growth factor; heparin binding; kringle

  Query Match             21.2%;  Score 29;  DB 2;  Length 24;
  Best Local Similarity   44.4%;  Pred. No. 1.3e+03;
  Matches    4;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ALKWKNAHL 12
              :||::| |:
Db         16 SLKYRNKHI 24


RESULT 7
I38253
T-cell acute lymphocytic leukemia 1 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
C;Accession: I38253
R;Chen, Q.; Yang, C.Y.; Tsan, J.T.; Xia, Y.; Ragab, A.H.; Peiper, S.C.; Carroll, A.; Bae
J. Exp. Med. 172, 1403-1408, 1990
A;Title: Coding sequences of the tal-1 gene are disrupted by chromosome translocation in
A;Reference number: I38253; MUID:91037802; PMID:2230650
A;Accession: I38253
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-24 <RES>
A;Cross-references: EMBL:X58621; NID:g36683; PIDN:CAA41476.1; PID:g36684
C;Genetics:
A;Gene: GDB:TAL1; SCL; TCL5
A;Cross-references: GDB:120759; OMIM:187040
A;Map position: 1p32-1p32

  Query Match             21.2%;  Score 29;  DB 2;  Length 24;
  Best Local Similarity   55.6%;  Pred. No. 1.3e+03;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 RALKWKNAH 11
              || || :|:
Db         10 RASKWPHAY 18


RESULT 8
A53592
H+-exporting ATPase (EC 3.6.3.6) 24k chain - Thermus aquaticus (fragment)
C;Species: Thermus aquaticus
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: A53592
R;Yokoyama, K.; Akabane, Y.; Ishii, N.; Yoshida, M.
J. Biol. Chem. 269, 12248-12253, 1994
A;Title: Isolation of prokaryotic V-0V-1-ATPase from a thermophilic eubacterium Thermus
A;Reference number: A53592; MUID:94216345; PMID:8163530
A;Accession: A53592
```

```
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <YOK>
A;Cross-references: UNIPROT:Q7M196
C;Keywords: hydrolase

  Query Match             20.8%;  Score 28.5;  DB 2;  Length 20;
  Best Local Similarity   52.6%;  Pred. No. 1.2e+03;
  Matches   10;  Conservative    1;  Mismatches    5;  Indels    3;  Gaps    1;

Qy         10 AHLKQEIAALEQEIAALEQ 28
              | | ||:   | || || |
Db          5 AILSQEV---EAEIQALLQ 20


RESULT 9
S00495
hemocyanin chain III - Japanese spiny lobster (fragment)
C;Species: Panulirus japonicus (Japanese spiny lobster)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: S00495
R;Makino, N.; Kimura, S.
Eur. J. Biochem. 173, 423-430, 1988
A;Title: Subunits of Panulirus japonicus hemocyanin. 1. Isolation and properties.
A;Reference number: S00492; MUID:88196131; PMID:3360019
A;Accession: S00495
A;Molecule type: protein
A;Residues: 1-19 <MAK>
A;Cross-references: UNIPROT:P82313
C;Superfamily: hemocyanin
C;Keywords: copper; hemolymph; hexamer; oxygen carrier

  Query Match             20.4%;  Score 28;  DB 2;  Length 19;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+03;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 NAHLKQEI 16
              ||| :|:|
Db          7 NAHKQQDI 14


RESULT 10
C47689
flagellar core protein, 34K - Treponema hyodysenteriae (fragment)
C;Species: Treponema hyodysenteriae
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: C47689
R;Koopman, M.B.; Baats, E.; van Vorstenbosch, C.J.; van der Zeijst, B.A.; Kusters, J.G.
J. Gen. Microbiol. 138, 2697-2706, 1992
A;Title: The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are composed o
A;Reference number: A47689; MUID:93139764; PMID:1487733
A;Contents: C5, Treponema
A;Accession: C47689
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-24 <KOO>
A;Cross-references: UNIPROT:Q7M132
A;Note: sequence extracted from NCBI backbone (NCBIP:123402)

  Query Match             20.4%;  Score 28;  DB 2;  Length 24;
  Best Local Similarity   45.5%;  Pred. No. 1.7e+03;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 RALKWKNAHLK 13
              | ||:: |  |:
Db         14 RTLKFRNVDLR 24


RESULT 11
G61002
transformation-sensitive protein IEF-3613 - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: G61002
R;Bauw, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; C
Electrophoresis 11, 528-536, 1990
A;Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequenci
A;Reference number: A61002; MUID:91031404; PMID:1699755
A;Accession: G61002
A;Molecule type: protein
A;Residues: 1-27 <BAU>
A;Note: this material corresponds to transformed epithelial amnion cell (AMA) database p

  Query Match             20.4%;  Score 28;  DB 2;  Length 27;
  Best Local Similarity   31.2%;  Pred. No. 2e+03;
  Matches    5;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          8 KNAHLKQEIAALEQEI 23
              | |::  :: |||: :
Db          6 KLAYINPDLLALEETL 21


RESULT 12
A59325
probable bacteriophage receptor BactA [imported] - Bacteroides fragilis (fragment)
C;Species: Bacteroides fragilis
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C;Accession: A59325
R;Frias-Lopez, J.
submitted to the Protein Sequence Database, July 2000
A;Description: Identification of cell wall proteins of Bacteroides fragilis to which bac
A;Reference number: A59325
A;Accession: A59325
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-21 <FRI>
A;Cross-references: UNIPROT:Q7M123
A;Experimental source: strain ATCC 51477
A;Note: putative receptor for bacteriophage B40-8

  Query Match             19.7%;  Score 27;  DB 2;  Length 21;
  Best Local Similarity   58.3%;  Pred. No. 2.1e+03;
  Matches    7;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         15 EIAALEQEIAAL 26
              | |||  |: ||
Db          8 EPAALHDEMLAL 19


RESULT 13
PQ0844
DNA-binding protein AcBBP1 - Azorhizobium caulinodans (fragment)
C;Species: Azorhizobium caulinodans
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: PQ0844
R;Welters, P.; Metz, B.; Felix, G.; Palme, K.; Szczyglowski, K.; de Bruijn, F.J.
Plant Physiol. 102, 1095-1107, 1993
A;Title: Interaction of a rhizobial DNA-binding protein with the promoter region of a pl
A;Reference number: PQ0844; MUID:94105338; PMID:8278541
A;Accession: PQ0844
A;Molecule type: protein
A;Residues: 1-27 <WEL>
A;Cross-references: UNIPROT:Q7M1A8
A;Experimental source: strain ORS571

  Query Match             19.3%;  Score 26.5;  DB 2;  Length 27;
  Best Local Similarity   30.4%;  Pred. No. 3.1e+03;
  Matches    7;  Conservative    7;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          2 IRALKWKN-AHLKQEIAALEQEI 23
              :| |  :| | |:||   ::::
Db          3 MRKLVGRNFARLRQEKGLTQEDV 25


RESULT 14
PA0036
```

glycine cleavage system protein H1 and H2 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: PA0036
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensiona
A;Reference number: PA0001
A;Accession: PA0036
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Cross-references: UNIPROT:Q7M1X0
A;Experimental source: stem

  Query Match 19.0%; Score 26; DB 2; Length 15;
  Best Local Similarity 40.0%; Pred. No. 2e+03;
  Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 IRALKWKNAH 11
              :  ||: | |
Db          4 LEGLKYANCH 13
```

RESULT 15
PN0467
nitrogenase (EC 1.18.6.1) molybdenum-iron protein alpha chain - Azotobacter chroococcum
C;Species: Azotobacter chroococcum
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: PN0467
R;Jones, R.; Woodley, P.; Birkmann-Zinoni, A.; Robson, R.L.
Gene 123, 145-146, 1993
A;Title: The nifH gene encoding the Fe protein Component of the molybdenum nitrogenase f
A;Reference number: JN0516; MUID:93138425; PMID:8423000
A;Accession: PN0467
A;Molecule type: DNA
A;Residues: 1-19 <JON>
A;Cross-references: UNIPROT:Q43964; GB:M73020; NID:g142326; PIDN:AAA22141.1; PID:g289238
C;Genetics:
A;Gene: nifD
C;Superfamily: dinitrogenase alpha chain; nitrogenase vanadium-iron protein alpha chain
C;Keywords: ATP; nitrogen fixation; oxidoreductase

  Query Match 19.0%; Score 26; DB 2; Length 19;
  Best Local Similarity 36.4%; Pred. No. 2.5e+03;
  Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```
Qy         13 KQEIAALEQEI 23
              ::|: :| ||:
Db          6 REEVESLIQEV 16
```

Search completed: April 27, 2005, 15:07:13
Job time : 29.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2005, 14:46:25 ; Search time 112 Seconds
(without alignments)
128.020 Million cell updates/sec

Title: US-10-088-417A-4
Perfect score: 137
Sequence: 1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 23310

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	26.3	25	2	Q7M386	Q7m386 sus scrofa
2	34	24.8	27	2	Q661K4	Q661k4 borrelia ga
3	33	24.1	24	2	Q9RP49	Q9rp49 mycobacteri
4	32	23.4	25	2	Q7QXH6	Q7qxh6 giardia lam
5	32	23.4	26	2	Q9T2S3	Q9t2s3 solanum tub
6	31	22.6	16	2	Q9QW74	Q9qw74 mus sp. hom
7	31	22.6	21	2	Q63076	Q63076 rattus norv
8	31	22.6	22	2	Q9H002	Q9h002 homo sapien
9	30	21.9	22	2	Q7M0N2	Q7m0n2 yersinia ps
10	30	21.9	28	2	Q9IN95	Q9in95 human immun
11	29.5	21.5	28	2	Q6V4K8	Q6v4k8 streptococc
12	29	21.2	13	2	Q50038	Q50038 mycobacteri
13	29	21.2	23	2	Q6V106	Q6v106 mus spretus
14	29	21.2	24	1	HPTA_RABIT	P13571 oryctolagus
15	29	21.2	26	2	Q6BDL1	Q6bdl1 tricholoma
16	28.5	20.8	20	2	Q7M196	Q7m196 thermus aqu
17	28	20.4	19	1	HCY3_PANJA	P82313 panulirus j
18	28	20.4	21	2	Q9UCJ6	Q9ucj6 homo sapien
19	28	20.4	23	1	NIFD_ANASL	P33177 anabaena sp
20	28	20.4	24	2	Q7M132	Q7m132 treponema h
21	28	20.4	25	1	LYT1_HOGCA	P61507 hogna carol
22	27.5	20.1	27	2	Q8T3I7	Q8t3i7 drosophila
23	27	19.7	19	2	Q9BDG4	Q9bdg4 bos taurus
24	27	19.7	21	2	Q7M123	Q7m123 bacteroides
25	27	19.7	22	2	O44710	O44710 drosophila
26	27	19.7	23	2	Q94XD3	Q94xd3 pteroxanium
27	27	19.7	23	2	Q9AJQ7	Q9ajq7 vibrio fisc
28	27	19.7	24	2	Q9R1M2	Q9r1m2 rattus norv
29	27	19.7	26	2	Q9NJR1	Q9njr1 euprymna sc
30	26.5	19.3	27	2	Q7M1A8	Q7m1a8 azorhizobiu
31	26	19.0	13	2	Q9QW45	Q9qw45 rattus sp.
32	26	19.0	15	2	P82665	P82665 bos taurus
33	26	19.0	15	2	Q7M1X0	Q7m1x0 arabidopsis
34	26	19.0	18	2	Q9QZX4	Q9qzx4 mus spretus
35	26	19.0	18	2	Q9QZX5	Q9qzx5 mus musculu
36	26	19.0	19	2	Q43964	Q43964 azotobacter
37	26	19.0	20	2	Q9TWN5	Q9twn5 theileria s
38	26	19.0	20	2	Q7LZ13	Q7lz13 gallus gall
39	26	19.0	23	2	Q9UCS1	Q9ucs1 homo sapien
40	26	19.0	23	2	Q6QNW3	Q6qnw3 anthopleura
41	26	19.0	23	2	Q6QNW4	Q6qnw4 anthopleura
42	26	19.0	23	2	Q6QNX4	Q6qnx4 anthopleura
43	26	19.0	24	2	Q9R5S2	Q9r5s2 lactobacill
44	26	19.0	25	1	FLB1_TREHY	P80158 treponema h
45	26	19.0	25	1	RL41_ICTPU	Q90ys7 ictalurus p

ALIGNMENTS

RESULT 1
Q7M386
ID Q7M386 PRELIMINARY; PRT; 25 AA.
AC Q7M386;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calpain II heavy chain.
OS Sus scrofa domestica (domestic pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9825;
RN [1]
RP SEQUENCE.
RA Crawford C., Brown N.R., Willis A.C.;
RT "Studies of the active site of m-calpain and the interaction with
RT calpastatin.";
RL Biochem. J. 296:135-142(1993).
DR PIR; S39391; S39391.
SQ SEQUENCE 25 AA; 2966 MW; 946A6DB2820F58A7 CRC64;

Query Match 26.3%; Score 36; DB 2; Length 25;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 7; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

```
Qy          3 RALKWKNAHLKQEIAALEQEI 23
              ||:|: |:  | :   :: ||
Db          4 RAVKYLNSEKKADYQVVDDEI 24
```

RESULT 2
Q661K4
ID Q661K4 PRELIMINARY; PRT; 27 AA.
AC Q661K4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BG0417;
OS Borrelia garinii PBi.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=290434;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PBi;
RA Gloeckner G., Lehmann R., Romualdi A., Pradella S.,
RA Schulte-Spechtel U., Wilske B., Suehnel J., Platzer M.;
RT "Comparative analysis of the Borrelia garinii genome.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; CP000013; AAU07267.1; -.
KW Hypothetical protein.
SQ SEQUENCE 27 AA; 3278 MW; F2F1EE4EDE3D9083 CRC64;

Query Match 24.8%; Score 34; DB 2; Length 27;

```
  Best Local Similarity   52.9%;  Pred. No. 2.2e+03;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIA 17
              || ||| || : |  |:
Db          4 KILALKKKNLNYKINIS 20


RESULT 3
Q9RP49
ID   Q9RP49      PRELIMINARY;      PRT;    24 AA.
AC   Q9RP49;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Putative glycogen phosphorylase GlgP (Fragment).
GN   Name=glgP;
OS   Mycobacterium smegmatis.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1772;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mc2155;
RX   MEDLINE=20011333; PubMed=10542168;
RA   Belanger A.E., Hatfull G.F.;
RT   "Exponential-phase glycogen recycling is essential for growth of
RT   Mycobacterium smegmatis.";
RL   J. Bacteriol. 181:6670-6678(1999).
DR   EMBL; AF172946; AAF07897.1; -.
FT   NON_TER     24     24
SQ   SEQUENCE   24 AA;  2865 MW;  0DB1CFD072F8A36B CRC64;

  Query Match             24.1%;  Score 33;  DB 2;  Length 24;
  Best Local Similarity   54.5%;  Pred. No. 2.6e+03;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 HLKQEIAALEQ 21
              || : :||||:
Db         12 HLPERLAALER 22


RESULT 4
Q7QXH6
ID   Q7QXH6      PRELIMINARY;      PRT;    25 AA.
AC   Q7QXH6;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   GLP_14_5818_5741.
OS   Giardia lamblia ATCC 50803.
OC   Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX   NCBI_TaxID=184922;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WB C6;
RA   Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA   Olsen G.J., Sogin M.L.;
RT   "Draft sequence of the Giardia lamblia genome.";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACB01000060; EAA39724.1; -.
DR   GO; GO:0005840; C:ribosome; IEA.
DR   GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR   GO; GO:0006412; P:protein biosynthesis; IEA.
DR   InterPro; IPR007836; Ribosomal_L41.
DR   Pfam; PF05162; Ribosomal_L41; 1.
SQ   SEQUENCE   25 AA;  3267 MW;  9AD629C253733C4E CRC64;

  Query Match             23.4%;  Score 32;  DB 2;  Length 25;
  Best Local Similarity   46.2%;  Pred. No. 3.7e+03;
  Matches    6;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLK 13
              ::| || |  |:|
Db          9 RMRKLKRKRRHMK 21


RESULT 5
Q9T2S3
ID   Q9T2S3      PRELIMINARY;      PRT;    26 AA.
AC   Q9T2S3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Cytochrome-C reductase 55 kDa subunit (EC 1.10.2.2) (Fragment).
OS   Solanum tuberosum (Potato).
OG   Mitochondrion.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Solanum.
OX   NCBI_TaxID=4113;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94198758; PubMed=7764624;
RA   Braun H.P., Kruft V., Schmitz U.K.;
RL   Planta 193:99-106(1994).
DR   MEROPS; M16.003; -.
DR   GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR   GO; GO:0008121; F:ubiquinol-cytochrome-c reductase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001431; Insulinase_like.
DR   Pfam; PF00675; Peptidase_M16; 1.
SQ   SEQUENCE   26 AA;  3042 MW;  C92C5787C8F12AC8 CRC64;

  Query Match             23.4%;  Score 32;  DB 2;  Length 26;
  Best Local Similarity   63.6%;  Pred. No. 3.9e+03;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 KQEIAALEQEI 23
              |: | |||:||
Db          1 KRPIRALEEEI 11


RESULT 6
Q9QW74
ID   Q9QW74      PRELIMINARY;      PRT;    16 AA.
AC   Q9QW74;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Homeobox GSH-5 (Fragment).
OS   Mus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10095;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92073356; PubMed=1683707;
RA   Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
RA   Copeland N.G., Potter S.S.;
RT   "Identification of 10 murine homeobox genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR009057; Homeodomain_like.
DR   ProDom; PD000010; Homeobox; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
KW   DNA-binding; Homeobox; Nuclear protein.
FT   NON_TER      1      1
FT   NON_TER     16     16
```

```
SQ   SEQUENCE   16 AA;  2178 MW;  AEC306578EE24361 CRC64;

  Query Match             22.6%;  Score 31;  DB 2;  Length 16;
  Best Local Similarity   50.0%;  Pred. No. 3.1e+03;
  Matches    4;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RALKWKNA 10
              | :||:|:
Db          8 RRMKWRNS 15


RESULT 7
Q63076
ID   Q63076      PRELIMINARY;      PRT;    21 AA.
AC   Q63076;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alpha-2 type I collagen (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal calvaria;
RX   MEDLINE=85122694; PubMed=6395893;
RA   Genovese C., Rowe D., Kream B.;
RT   "Construction of DNA sequences complementary to rat alpha 1 and alpha
RT   2 collagen mRNA and their use in studying the regulation of type I
RT   collagen synthesis by 1,25-dihydroxyvitamin D.";
RL   Biochemistry 23:6210-6216(1984).
DR   EMBL; M12200; AAA40835.1; -.
DR   PIR; I65270; I65270.
DR   GO; GO:0005581; C:collagen; IEA.
DR   GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR   InterPro; IPR000885; Fib_collagen_C.
DR   Pfam; PF01410; COLFI; 1.
DR   ProDom; PD002078; Fib_collagen_C; 1.
KW   Collagen.
FT   NON_TER       1      1
FT   NON_TER      21     21
SQ   SEQUENCE   21 AA;  2358 MW;  B86A6ECCEEE46D60 CRC64;

  Query Match             22.6%;  Score 31;  DB 2;  Length 21;
  Best Local Similarity   50.0%;  Pred. No. 4.2e+03;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         11 HLKQEIAALEQE 22
              | |  || |::|
Db          8 HCKNSIAYLDEE 19


RESULT 8
Q9H002
ID   Q9H002      PRELIMINARY;      PRT;    22 AA.
AC   Q9H002;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ATP-binding cassette transporter-1 (Fragment).
GN   Name=ABC-1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Porsch-Oezcueruemez M., Langmann T., Schmitz G.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Porsch-Oezcueruemez M.K.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ252277; CAC21428.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
KW   ATP-binding.
FT   NON_TER      22     22
SQ   SEQUENCE   22 AA;  2831 MW;  6183559EA0C22B53 CRC64;

  Query Match             22.6%;  Score 31;  DB 2;  Length 22;
  Best Local Similarity   55.6%;  Pred. No. 4.4e+03;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKN 9
              ::| | |||
Db          6 QLRLLLWKN 14


RESULT 9
Q7M0N2
ID   Q7M0N2      PRELIMINARY;      PRT;    22 AA.
AC   Q7M0N2;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Unidentified low M-r protein (Fragment).
OS   Yersinia pseudotuberculosis.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Yersinia.
OX   NCBI_TaxID=633;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=90243678; PubMed=2159466;
RA   Han O., Miller V.P., Liu H.;
RT   "Mechanistic studies of the biosynthesis of 3,6-dideoxyhexoses in
RT   Yersinia pseudotuberculosis. Purification and characterization of CDP-
RT   6-deoxy-delta(3,4)-glucoseen reductase based on its
RT   NADH:dichlorophenolindolphenol oxidoreductase activity.";
RL   J. Biol. Chem. 265:8033-8041(1990).
DR   PIR; B35372; B35372.
FT   NON_TER      22     22
SQ   SEQUENCE   22 AA;  2192 MW;  3E88CD8AAC8680BB CRC64;

  Query Match             21.9%;  Score 30;  DB 2;  Length 22;
  Best Local Similarity   70.0%;  Pred. No. 5.9e+03;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         17 AALEQEIAAL 26
              ||| :|:|||
Db          6 AALVKELAAL 15


RESULT 10
Q9IN95
ID   Q9IN95      PRELIMINARY;      PRT;    28 AA.
AC   Q9IN95;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Gag protein (Fragment).
GN   Name=gag;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99260287; PubMed=10331444; DOI=10.1089/088922299310953;
RA   Mokili J.L., Wade C.M., Burns S.M., Cutting W.A., Bopopi J.M.,
RA   Green S.D., Peutherer J.F., Simmonds P.;
RT   "Genetic heterogeneity of HIV type 1 subtypes in Kimpese, rural
RT   Democratic Republic of Congo.";
RL   AIDS Res. Hum. Retroviruses 15:655-664(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Mokili J.L.K.;
```

```
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF144854; AAF69080.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   28 AA;  3322 MW;  76748DCB3296BAA9 CRC64;

  Query Match             21.9%;  Score 30;  DB 2;  Length 28;
  Best Local Similarity   66.7%;  Pred. No. 7.6e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 WKNAHL 12
              ||::||
Db          2 WKDSHL 7


RESULT 11
Q6V4K8
ID   Q6V4K8      PRELIMINARY;      PRT;    28 AA.
AC   Q6V4K8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   M protein (Fragment).
OS   Streptococcus pyogenes.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1314;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NS696;
RX   PubMed=14688117; DOI=10.1128/IAI.72.1.364-370.2004;
RA   McKay F.C., McArthur J.D., Sanderson-Smith M.L., Gardam S.,
RA   Currie B.J., Sriprakash K.S., Fagan P.K., Towers R.J., Batzloff M.R.,
RA   Chhatwal G.S., Ranson M., Walker M.J.;
RT   "Plasminogen binding by group A streptococcal isolates from a region
RT   of hyperendemicity for streptococcal skin infection and a high
RT   incidence of invasive infection.";
RL   Infect. Immun. 72:364-370(2004).
DR   EMBL; AY351858; AAQ64528.1; -.
FT   NON_TER       1      1
FT   NON_TER      28     28
SQ   SEQUENCE   28 AA;  3463 MW;  013B1C94B01B96ED CRC64;

  Query Match             21.5%;  Score 29.5;  DB 2;  Length 28;
  Best Local Similarity   38.1%;  Pred. No. 8.8e+03;
  Matches    8;  Conservative    4;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 WKNAHLKQEIAALEQEIAALE 27
              |    |::|   ||::  |||
Db          1 WDRQRLEKE---LEEKKEALE 18


RESULT 12
Q50038
ID   Q50038      PRELIMINARY;      PRT;    13 AA.
AC   Q50038;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE   U22661.
OS   Mycobacterium leprae.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1769;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Smith D.R.;
RL   Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Robison K.;
RL   Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U15182; AAA62970.1; -.
SQ   SEQUENCE   13 AA;  1589 MW;  C7CCD7E47D025B06 CRC64;

  Query Match             21.2%;  Score 29;  DB 2;  Length 13;
  Best Local Similarity   45.5%;  Pred. No. 4.6e+03;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 HLKQEIAALEQ 21
              |::||   :||
Db          3 HVQQEYLGVEQ 13


RESULT 13
Q6V106
ID   Q6V106      PRELIMINARY;      PRT;    23 AA.
AC   Q6V106;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Heme oxygenase 1 (Fragment).
GN   Name=Ho1;
OS   Mus spretus (Western wild mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10096;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Cabrera-Luque J.M., Prieto-Alamo M.J., Pueyo C.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY355145; AAQ55831.1; -.
FT   NON_TER       1      1
FT   NON_TER      23     23
SQ   SEQUENCE   23 AA;  2852 MW;  F8D0C3F6975C5900 CRC64;

  Query Match             21.2%;  Score 29;  DB 2;  Length 23;
  Best Local Similarity   75.0%;  Pred. No. 8.3e+03;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 AALEQEIA 24
              |||||::|
Db          4 AALEQDMA 11


RESULT 14
HPTA_RABIT
ID   HPTA_RABIT      STANDARD;      PRT;    24 AA.
AC   P13571;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Heptapoietin A light chain (HPTA) (Fragment).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=89392048; PubMed=2528955;
RA   Zarnegar R., Muga S., Enghild J., Michalopoulos G.;
RT   "NH2-terminal amino acid sequence of rabbit hepatopoietin A, a
RT   heparin-binding polypeptide growth factor for hepatocytes.";
RL   Biochem. Biophys. Res. Commun. 163:1370-1376(1989).
CC   -!- FUNCTION: HPTA is an acidic heparin-binding growth factor for
CC       hepatocytes.
CC   -!- SUBUNIT: Heterodimer of an heavy and a light chain linked by
CC       disulfide bond(s).
DR   PIR; A33262; A33262.
KW   Direct protein sequencing; Growth factor; Heparin-binding.
FT   NON_TER      24     24
SQ   SEQUENCE   24 AA;  2768 MW;  E78BBF9B807262FE CRC64;

  Query Match             21.2%;  Score 29;  DB 1;  Length 24;
  Best Local Similarity   44.4%;  Pred. No. 8.7e+03;
  Matches    4;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          4 ALKWKNAHL 12
              :||::| |:
Db         16 SLKYRNKHI 24


RESULT 15
Q6BDL1
ID   Q6BDL1      PRELIMINARY;      PRT;    26 AA.
AC   Q6BDL1;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Tricholoma matsutake.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Agaricales; Tricholomataceae; Tricholoma.
OX   NCBI_TaxID=40145;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Murata H.;
RT   "Characterization of the insertion sites of marY1, the gypsy-type
RT   retrotransposon from the ectomycorrhizal basidiomycete Tricholoma
RT   matsutake strain Y1, in the genome the fungus based on the inter-
RT   retrotransposon amplified polymorphism analysis.";
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR   EMBL; AB160891; BAD32667.1; -.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003682; F:chromatin binding; IEA.
DR   GO; GO:0006333; P:chromatin assembly or disassembly; IEA.
DR   InterPro; IPR000953; Chromo.
DR   Pfam; PF00385; Chromo; 1.
DR   PROSITE; PS00598; CHROMO_1; UNKNOWN_1.
DR   PROSITE; PS50013; CHROMO_2; 1.
KW   Hypothetical protein; Nuclear protein.
FT   NON_TER       1      1
FT   NON_TER      26     26
SQ   SEQUENCE   26 AA;  3272 MW;  3E4B000853591617 CRC64;

  Query Match             21.2%;  Score 29;  DB 2;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 9.4e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 LKWKN 9
              :||||
Db          7 IKWKN 11


Search completed: April 27, 2005, 15:06:18
Job time : 114 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2005, 14:58:17 ; Search time 29.5 Seconds
(without alignments)
70.853 Million cell updates/sec

Title: US-10-088-417A-4
Perfect score: 137
Sequence: 1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 228236

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	34.3	21	4	US-09-834-759-534	Sequence 534, App
2	45	32.8	26	4	US-09-403-861A-8	Sequence 8, Appli
3	45	32.8	27	2	US-07-684-965-9	Sequence 9, Appli
4	45	32.8	27	3	US-09-252-658-9	Sequence 9, Appli
5	45	32.8	28	3	US-08-486-099-84	Sequence 84, Appl
6	45	32.8	28	3	US-08-360-107A-94	Sequence 94, Appl
7	45	32.8	28	3	US-08-484-223B-84	Sequence 84, Appl
8	45	32.8	28	3	US-08-919-597-84	Sequence 84, Appl
9	45	32.8	28	3	US-08-475-668A-84	Sequence 84, Appl
10	45	32.8	28	3	US-08-485-551A-84	Sequence 84, Appl
11	45	32.8	28	3	US-08-471-913A-84	Sequence 84, Appl
12	45	32.8	28	3	US-08-485-264A-84	Sequence 84, Appl
13	45	32.8	28	3	US-08-474-349A-84	Sequence 84, Appl
14	45	32.8	28	4	US-08-255-208A-20	Sequence 20, Appl
15	45	32.8	28	4	US-08-470-896-84	Sequence 84, Appl
16	45	32.8	28	4	US-09-914-259-1	Sequence 1, Appli
17	45	32.8	28	4	US-08-485-546A-84	Sequence 84, Appl
18	45	32.8	28	4	US-09-350-841A-1549	Sequence 1549, Ap
19	45	32.8	28	4	US-09-350-841A-1566	Sequence 1566, Ap
20	45	32.8	28	4	US-09-350-841A-1573	Sequence 1573, Ap
21	45	32.8	28	4	US-08-487-266A-84	Sequence 84, Appl
22	44	32.1	24	4	US-09-491-614B-29	Sequence 29, Appl
23	44	32.1	28	1	US-08-182-175A-1	Sequence 1, Appli
24	44	32.1	28	5	PCT-US92-06412-1	Sequence 1, Appli
25	43	31.4	24	2	US-08-491-527A-12	Sequence 12, Appl
26	42	30.7	24	2	US-08-491-527A-11	Sequence 11, Appl
27	42	30.7	25	4	US-09-491-614B-25	Sequence 25, Appl
28	42	30.7	26	2	US-08-690-011A-37	Sequence 37, Appl
29	42	30.7	26	3	US-09-299-495F-37	Sequence 37, Appl
30	40	29.2	14	2	US-08-491-527A-8	Sequence 8, Appli
31	39	28.5	22	3	US-09-248-588-98	Sequence 98, Appl
32	38	27.7	14	2	US-08-491-527A-9	Sequence 9, Appli
33	38	27.7	25	2	US-08-690-011A-2	Sequence 2, Appli
34	38	27.7	25	3	US-09-299-495F-2	Sequence 2, Appli
35	38	27.7	26	2	US-08-690-011A-3	Sequence 3, Appli
36	38	27.7	26	3	US-09-299-495F-3	Sequence 3, Appli
37	38	27.7	28	1	US-08-182-175A-3	Sequence 3, Appli
38	38	27.7	28	1	US-08-474-633A-70	Sequence 70, Appl
39	38	27.7	28	4	US-08-823-771-70	Sequence 70, Appl
40	38	27.7	28	5	PCT-US92-06412-3	Sequence 3, Appli
41	37	27.0	27	2	US-07-684-965-8	Sequence 8, Appli
42	37	27.0	27	3	US-09-252-658-8	Sequence 8, Appli
43	37	27.0	28	1	US-07-977-630-53	Sequence 53, Appl
44	36	26.3	14	2	US-08-491-527A-7	Sequence 7, Appli
45	36	26.3	14	2	US-08-491-527A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-834-759-534
; Sequence 534, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 534
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-534

Query Match 34.3%; Score 47; DB 4; Length 21;
Best Local Similarity 57.9%; Pred. No. 5.8;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```
Qy          9 NAHLKQEIAALEQEIAALE 27
              |  ||:|||  |: |||  |:
Db          1 NCMLKKEIAMLKLEIATLK 19
```

RESULT 2
US-09-403-861A-8
; Sequence 8, Application US/09403861A
; Patent No. 6833348
; GENERAL INFORMATION:
; APPLICANT: RICCARDI, Carlo
; TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL
; DEATH PATHWAYS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001

```
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/403,861A
;            FILING DATE: 11-Feb-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/EP98/02490
;            FILING DATE: 27-APR-1998
;            APPLICATION NUMBER: EP 97107033.9
;            FILING DATE: 28-APR-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: YUN, Allen C.
;            REGISTRATION NUMBER: 37,971
;            REFERENCE/DOCKET NUMBER: RICCARDI=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 26 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-403-861A-8

  Query Match             32.8%;  Score 45;  DB 4;  Length 26;
  Best Local Similarity   42.9%;  Pred. No. 14;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          4 KVEELLSKNYHLENEVARLKK 24


RESULT 3
US-07-684-965-9
; Sequence 9, Application US/07684965
; Patent No. 5919649
;  GENERAL INFORMATION:
;    APPLICANT:  HABENER, JOEL F.
;    APPLICANT:  HOEFFLER, JAMES P.
;    TITLE OF INVENTION:  A-CAMP RESPONSIVE TRANSCRIPTIONAL
;    TITLE OF INVENTION:  ENHANCER BINDING PROTEIN
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1225 Connecticut Avenue, N.W., Suite 300
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/684,965
;      FILING DATE:  19910522
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0609.2470004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)833-7533
;      TELEFAX:  (202)833-8716
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-684-965-9

  Query Match             32.8%;  Score 45;  DB 2;  Length 27;
  Best Local Similarity   42.9%;  Pred. No. 14;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          4 KVEELLSKNYHLENEVARLKK 24


RESULT 4
US-09-252-658-9
; Sequence 9, Application US/09252658
; Patent No. 6251667
;  GENERAL INFORMATION:
;    APPLICANT:  HABENER, JOEL F.
;    APPLICANT:  HOEFFLER, JAMES P.
;    TITLE OF INVENTION:  A cAMP-RESPONSIVE TRANSCRIPTIONAL
;    TITLE OF INVENTION:  ENHANCER BINDING PROTEIN
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., NW, STE. 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/252,658
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/684,965
;      FILING DATE:  22-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US89/05234
;      FILING DATE:  20-NOV-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/272,980
;      FILING DATE:  18-NOV-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0609.1990002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)371-2600
;      TELEFAX:  (202)371-2540
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-252-658-9

  Query Match             32.8%;  Score 45;  DB 3;  Length 27;
  Best Local Similarity   42.9%;  Pred. No. 14;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
```

```
Db          4 KVEELLSKNYHLENEVARLKK 24


RESULT 5
US-08-486-099-84
; Sequence 84, Application US/08486099
; Patent No. 6013263
;  GENERAL INFORMATION:
;    APPLICANT:  Bolognesi, Dani P.
;    APPLICANT:  Matthews, Thomas J.
;    APPLICANT:  Wild, Carl T.
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway, Stephen R.
;    APPLICANT:  Langlois, Alphonse J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR INHIBITION OF
;    TITLE OF INVENTION:  MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
;    TITLE OF INVENTION:  B VIRUS TRANSMISSION
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,099
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-031
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-486-099-84

  Query Match             32.8%;  Score 45;  DB 3;  Length 28;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          7 KVEELLSKNYHLENEVARLKK 27


RESULT 6
US-08-360-107A-94
; Sequence 94, Application US/08360107A
; Patent No. 6017536
;  GENERAL INFORMATION:
;    APPLICANT:  Bolognesi, Dani P.
;    APPLICANT:  Matthews, Thomas J.
;    APPLICANT:  Wild, Carl T.
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway, Stephen R.
;    APPLICANT:  Langlois, Alphonse J.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR INHIBITION
;    TITLE OF INVENTION:  OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
;    TITLE OF INVENTION:  TRANSMISSION
;    NUMBER OF SEQUENCES:  149
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/360,107A
;      FILING DATE:  20-DEC-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-013
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  94:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-360-107A-94

  Query Match             32.8%;  Score 45;  DB 3;  Length 28;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          7 KVEELLSKNYHLENEVARLKK 27


RESULT 7
US-08-484-223B-84
; Sequence 84, Application US/08484223B
; Patent No. 6020459
;  GENERAL INFORMATION:
;    APPLICANT:  Bolognesi, Dani P.
;    APPLICANT:  Matthews, Thomas J.
;    APPLICANT:  Wild, Carl T.
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway, Stephen R.
;    APPLICANT:  Langlois, Alphonse J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR INHIBITION OF
;    TITLE OF INVENTION:  MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
;    TITLE OF INVENTION:  TRANSMISSION
;    NUMBER OF SEQUENCES:  245
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,223B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-029
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-484-223B-84

  Query Match             32.8%;  Score 45;  DB 3;  Length 28;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          7 KVEELLSKNYHLENEVARLKK 27


RESULT 8
US-08-919-597-84
; Sequence 84, Application US/08919597
; Patent No. 6054265
;  GENERAL INFORMATION:
;    APPLICANT:  Bolognesi, Dani P.
;    APPLICANT:  Matthews, Thomas J.
;    APPLICANT:  Wild, Carl T.
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway, Stephen R.
;    APPLICANT:  Langlois, Alphonse J.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR INHIBITION
;    TITLE OF INVENTION:  OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
;    TITLE OF INVENTION:  TRANSMISSION
;    NUMBER OF SEQUENCES:  273
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/919,597
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/470,896
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-020
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-919-597-84

  Query Match             32.8%;  Score 45;  DB 3;  Length 28;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          7 KVEELLSKNYHLENEVARLKK 27


RESULT 9
US-08-475-668A-84
; Sequence 84, Application US/08475668A
; Patent No. 6060065
;  GENERAL INFORMATION:
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway, Stephen R.
;    TITLE OF INVENTION:  COMPOSITIONS FOR INHIBITION OF MEMBRANE
;    TITLE OF INVENTION:  FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
;    TITLE OF INVENTION:  TRANSMISSION
;    NUMBER OF SEQUENCES:  211
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,668A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-026
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-475-668A-84

  Query Match             32.8%;  Score 45;  DB 3;  Length 28;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          7 KVEELLSKNYHLENEVARLKK 27
```

```
RESULT 10
US-08-485-551A-84
; Sequence 84, Application US/08485551A
; Patent No. 6068973
;  GENERAL INFORMATION:
;    APPLICANT:  Bolognesi, Dani P.
;    APPLICANT:  Matthews, Thomas J.
;    APPLICANT:  Wild, Carl T.
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway, Stephen R.
;    APPLICANT:  Langlois, Alphonse J.
;    TITLE OF INVENTION:  METHODS FOR INHIBITION OF MEMBRANE
;    TITLE OF INVENTION:  FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
;    TITLE OF INVENTION:  TRANSMISSION
;    NUMBER OF SEQUENCES:  211
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,551A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-023
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-485-551A-84

  Query Match             32.8%;  Score 45;  DB 3;  Length 28;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          7 KVEELLSKNYHLENEVARLKK 27


RESULT 11
US-08-471-913A-84
; Sequence 84, Application US/08471913A
; Patent No. 6093794
;  GENERAL INFORMATION:
;    APPLICANT:  Bolognesi, Dani P.
;    APPLICANT:  Matthews, Thomas J.
;    APPLICANT:  Wild, Carl T.
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway, Stephen R.
;    APPLICANT:  Langlois, Alphonse J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR INHIBITION OF MEMBRANE
;    TITLE OF INVENTION:  FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
;    TITLE OF INVENTION:  TRANSMISSION
;    NUMBER OF SEQUENCES:  214
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/471,913A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-471-913A-84

  Query Match             32.8%;  Score 45;  DB 3;  Length 28;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          7 KVEELLSKNYHLENEVARLKK 27


RESULT 12
US-08-485-264A-84
; Sequence 84, Application US/08485264A
; Patent No. 6228983
;  GENERAL INFORMATION:
;    APPLICANT:  Bolognesi, Dani P.
;    APPLICANT:  Matthews, Thomas J.
;    APPLICANT:  Wild, Carl T.
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway, Stephen R.
;    APPLICANT:  Langlois, Alphonse J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR INHIBITION OF
;    TITLE OF INVENTION:  MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
;    TITLE OF INVENTION:  RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
;    NUMBER OF SEQUENCES:  232
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,264A
```

```
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-021
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-485-264A-84

  Query Match             32.8%;  Score 45;  DB 3;  Length 28;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          7 KVEELLSKNYHLENEVARLKK 27


RESULT 13
US-08-474-349A-84
; Sequence 84, Application US/08474349A
; Patent No. 6333395
;  GENERAL INFORMATION:
;    APPLICANT:  Bolognesi, Dani P.
;    APPLICANT:  Matthews, Thomas J.
;    APPLICANT:  Wild, Carl T.
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway, Stephen R.
;    APPLICANT:  Langlois, Alphonse J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR INHIBITION OF MEMBRANE
;    TITLE OF INVENTION:  FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
;    TITLE OF INVENTION:  VIRUS TRANSMISSION
;    NUMBER OF SEQUENCES:  517
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,349A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-024
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-474-349A-84

  Query Match             32.8%;  Score 45;  DB 3;  Length 28;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          7 KVEELLSKNYHLENEVARLKK 27


RESULT 14
US-08-255-208A-20
; Sequence 20, Application US/08255208A
; Patent No. 6440656
;  GENERAL INFORMATION:
;    APPLICANT:  Bolognesi, Dani P.
;    APPLICANT:  Matthews, Thomas J.
;    APPLICANT:  Wild, Carl T.
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway Jr., Stephen R.
;    TITLE OF INVENTION:  SYNTHETIC PEPTIDE INHIBITORS OF HIV
;    TITLE OF INVENTION:  TRANSMISSION
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/255,208A
;      FILING DATE:  07-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-255-208A-20

  Query Match             32.8%;  Score 45;  DB 4;  Length 28;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          7 KVEELLSKNYHLENEVARLKK 27


RESULT 15
US-08-470-896-84
; Sequence 84, Application US/08470896
; Patent No. 6479055
;  GENERAL INFORMATION:
```

; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-470-896-84

Query Match 32.8%; Score 45; DB 4; Length 28;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          7 KVEELLSKNYHLENEVARLKK 27
```

Search completed: April 27, 2005, 15:19:43
Job time : 30.5 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2005, 15:02:43 ; Search time 89.5 Seconds
(without alignments)
104.113 Million cell updates/sec

Title: US-10-088-417A-4
Perfect score: 137
Sequence: 1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 334731

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	81	59.1	28	14	US-10-360-053-23	Sequence 23, Appl
2	59	43.1	28	14	US-10-360-053-21	Sequence 21, Appl
3	54	39.4	28	14	US-10-360-053-22	Sequence 22, Appl
4	51	37.2	24	14	US-10-338-083-19	Sequence 19, Appl
5	51	37.2	24	16	US-10-611-399-19	Sequence 19, Appl
6	51	37.2	24	17	US-10-794-751-19	Sequence 19, Appl
7	50	36.5	23	10	US-09-259-658-59	Sequence 59, Appl
8	47	34.3	21	9	US-09-834-759-534	Sequence 534, App
9	47	34.3	21	13	US-10-007-805-534	Sequence 534, App
10	47	34.3	21	13	US-10-007-805-587	Sequence 587, App
11	47	34.3	21	14	US-10-076-622-534	Sequence 534, App
12	47	34.3	21	14	US-10-076-622-587	Sequence 587, App
13	47	34.3	21	14	US-10-124-805-534	Sequence 534, App
14	47	34.3	21	14	US-10-124-805-587	Sequence 587, App
15	45	32.8	26	16	US-10-630-926-8	Sequence 8, Appli
16	45	32.8	28	14	US-10-080-608A-1	Sequence 1, Appli
17	45	32.8	28	15	US-10-370-685-90	Sequence 90, Appl
18	45	32.8	28	15	US-10-267-682-84	Sequence 84, Appl
19	45	32.8	28	15	US-10-267-748-84	Sequence 84, Appl
20	44	32.1	24	10	US-09-491-614-30	Sequence 30, Appl
21	43	31.4	20	14	US-10-076-622-596	Sequence 596, App
22	43	31.4	20	14	US-10-124-805-596	Sequence 596, App
23	42	30.7	26	14	US-10-059-720-37	Sequence 37, Appl
24	41	29.9	27	10	US-09-882-774-7	Sequence 7, Appli
25	39	28.5	17	14	US-10-210-023-111	Sequence 111, App
26	39	28.5	28	9	US-09-320-907B-6	Sequence 6, Appli
27	39	28.5	28	15	US-10-447-292-6	Sequence 6, Appli
28	38	27.7	25	14	US-10-059-720-2	Sequence 2, Appli
29	38	27.7	26	14	US-10-059-720-3	Sequence 3, Appli
30	38	27.7	28	14	US-10-023-066A-70	Sequence 70, Appl
31	38	27.7	28	16	US-10-804-678-70	Sequence 70, Appl
32	36	26.3	19	14	US-10-059-720-36	Sequence 36, Appl
33	36	26.3	24	14	US-10-059-720-1	Sequence 1, Appli
34	36	26.3	24	14	US-10-338-083-20	Sequence 20, Appl
35	36	26.3	24	16	US-10-611-399-20	Sequence 20, Appl
36	36	26.3	24	17	US-10-794-751-20	Sequence 20, Appl
37	36	26.3	28	14	US-10-023-066A-36	Sequence 36, Appl
38	36	26.3	28	14	US-10-023-066A-40	Sequence 40, Appl
39	36	26.3	28	14	US-10-023-066A-56	Sequence 56, Appl
40	36	26.3	28	14	US-10-023-066A-67	Sequence 67, Appl
41	36	26.3	28	16	US-10-804-678-36	Sequence 36, Appl
42	36	26.3	28	16	US-10-804-678-40	Sequence 40, Appl
43	36	26.3	28	16	US-10-804-678-56	Sequence 56, Appl
44	36	26.3	28	16	US-10-804-678-67	Sequence 67, Appl
45	35	25.5	20	14	US-10-225-567A-1341	Sequence 1341, Ap

ALIGNMENTS

RESULT 1
US-10-360-053-23
; Sequence 23, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenthal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibo
; TITLE OF INVENTION: Fragments via Antiparallel Hetergeneous Coiled-Coil Peptide Reg
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-23

Query Match 59.1%; Score 81; DB 14; Length 28;
Best Local Similarity 64.0%; Pred. No. 0.00084;
Matches 16; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 ALKWKNAHLKQEIAALEQEIAALEQ 28
              |:|:| | :| ||||::|||||:||
Db          1 AIKYKQAAIKNEIAAIKQEIAAIEQ 25
```

RESULT 2

US-10-360-053-21
; Sequence 21, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenthal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibo
; TITLE OF INVENTION: Fragments via Antiparallel Hetergeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-21

Query Match 43.1%; Score 59; DB 14; Length 28;
Best Local Similarity 40.0%; Pred. No. 0.69;
Matches 10; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 4 ALKWKNAHLKQEIAALEQEIAALEQ 28
|:::: | :|:||||:: :|||:::
Db 1 AIEYEQAAIKEEIAAIKDKIAAIKE 25

RESULT 3
US-10-360-053-22
; Sequence 22, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenthal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibo
; TITLE OF INVENTION: Fragments via Antiparallel Hetergeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-22

Query Match 39.4%; Score 54; DB 14; Length 28;
Best Local Similarity 50.0%; Pred. No. 3.2;
Matches 12; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KIRALKWKNAHLKQEIAALEQEIA 24
|| |:: | | :::|||| |::||
Db 5 KIAAIEEKIAQIEEEIAAQEEKIA 28

RESULT 4
US-10-338-083-19
; Sequence 19, Application US/10338083
; Publication No. US20030166559A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: coiled-coil motif
US-10-338-083-19

Query Match 37.2%; Score 51; DB 14; Length 24;
Best Local Similarity 55.6%; Pred. No. 6.7;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 10 AHLKQEIAALEQEIAALE 27
| |: |::||| |:|:||
Db 1 AALESEVSALESEVASLE 18

RESULT 5
US-10-611-399-19
; Sequence 19, Application US/10611399
; Publication No. US20040170602A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF
; FILE REFERENCE: A-71273-3
; CURRENT APPLICATION NUMBER: US/10/611,399
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: coiled-coil motif
US-10-611-399-19

Query Match 37.2%; Score 51; DB 16; Length 24;
Best Local Similarity 55.6%; Pred. No. 6.7;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 10 AHLKQEIAALEQEIAALE 27
| |: |::||| |:|:||
Db 1 AALESEVSALESEVASLE 18

RESULT 6
US-10-794-751-19
; Sequence 19, Application US/10794751
; Publication No. US20050048626A1
; GENERAL INFORMATION:

```
;  APPLICANT: Desjarlais, John R.
;  APPLICANT:  Thomason, Adam Read
;  APPLICANT:  Zhukovsky, Eugene Alexander
;  TITLE OF INVENTION: BAFF VARIANTS AND METHODS THEREOF
;  FILE REFERENCE: A-72175-1
;  CURRENT APPLICATION NUMBER: US/10/794,751
;  CURRENT FILING DATE:  2004-03-05
;  PRIOR APPLICATION NUMBER: US 10/338,083
;  PRIOR FILING DATE: 2003-01-06
;  PRIOR APPLICATION NUMBER: US 60/452,707
;  PRIOR FILING DATE: 2003-03-07
;  PRIOR APPLICATION NUMBER: US 60/482,081
;  PRIOR FILING DATE: 2003-06-23
;  PRIOR APPLICATION NUMBER: US 60/523,880
;  PRIOR FILING DATE: 2003-11-20
;  PRIOR APPLICATION NUMBER: US 60/528,104
;  PRIOR FILING DATE: 2003-12-08
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
;   LENGTH: 24
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: coiled-coil motif
US-10-794-751-19

  Query Match             37.2%;  Score 51;  DB 17;  Length 24;
  Best Local Similarity   55.6%;  Pred. No. 6.7;
  Matches   10;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 AHLKQEIAALEQEIAALE 27
              | |: |::||| |:|:||
Db          1 AALESEVSALESEVASLE 18


RESULT 7
US-09-259-658-59
; Sequence 59, Application US/09259658
; Publication No. US20030032054A1
; GENERAL INFORMATION:
;  APPLICANT:  Colyer
;  APPLICANT:  Craig
;  APPLICANT:  Maschio
;  APPLICANT:  Mezna
;  TITLE OF INVENTION:  Compositions And Methods For Monitoring The
;  TITLE OF INVENTION:  Modification State Of A Pair Of Polypeptides
;  FILE REFERENCE:  colyer 4256/79245
;  CURRENT APPLICATION NUMBER: US/09/259,658
;  CURRENT FILING DATE:  1999-02-26
;  NUMBER OF SEQ ID NOS:  59
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Synthetic
;   OTHER INFORMATION: peptide used to assay geranylgeranyl transferase
;   OTHER INFORMATION: activity.
US-09-259-658-59

  Query Match             36.5%;  Score 50;  DB 10;  Length 23;
  Best Local Similarity   56.5%;  Pred. No. 8.7;
  Matches   13;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          2 IRALKWKNAHLKQEIAALEQEIA 24
              |  || | | |||: | |:|:||
Db          1 IAQLKQKIAQLKQKNACLKQKIA 23


RESULT 8
US-09-834-759-534
; Sequence 534, Application US/09834759
; Publication No. US20020085998A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C9
;  CURRENT APPLICATION NUMBER: US/09/834,759
;  CURRENT FILING DATE:  2001-04-13
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 534
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-759-534

  Query Match             34.3%;  Score 47;  DB 9;  Length 21;
  Best Local Similarity   57.9%;  Pred. No. 20;
  Matches   11;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          9 NAHLKQEIAALEQEIAALE 27
              |  ||:||| |: ||| |:
Db          1 NCMLKKEIAMLKLEIATLK 19


RESULT 9
US-10-007-805-534
; Sequence 534, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Durham, Margarita
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C10
;  CURRENT APPLICATION NUMBER: US/10/007,805
;  CURRENT FILING DATE:  2001-12-07
;  NUMBER OF SEQ ID NOS: 593
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 534
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-007-805-534

  Query Match             34.3%;  Score 47;  DB 13;  Length 21;
  Best Local Similarity   57.9%;  Pred. No. 20;
  Matches   11;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          9 NAHLKQEIAALEQEIAALE 27
              |  ||:||| |: ||| |:
Db          1 NCMLKKEIAMLKLEIATLK 19


RESULT 10
US-10-007-805-587
; Sequence 587, Application US/10007805
```

```
; Publication No. US20020150581A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Durham, Margarita
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C10
;  CURRENT APPLICATION NUMBER: US/10/007,805
;  CURRENT FILING DATE:  2001-12-07
;  NUMBER OF SEQ ID NOS: 593
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 587
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-007-805-587

  Query Match             34.3%;  Score 47;  DB 13;  Length 21;
  Best Local Similarity   57.9%;  Pred. No. 20;
  Matches   11;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          9 NAHLKQEIAALEQEIAALE 27
              |  ||:||| |: ||| |:
Db          1 NCMLKKEIAMLKLEIATLK 19


RESULT 11
US-10-076-622-534
; Sequence 534, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
;  APPLICANT: Houghton, Raymond L.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Persing, David H.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C11
;  CURRENT APPLICATION NUMBER: US/10/076,622
;  CURRENT FILING DATE:  2002-02-13
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 534
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-076-622-534

  Query Match             34.3%;  Score 47;  DB 14;  Length 21;
  Best Local Similarity   57.9%;  Pred. No. 20;
  Matches   11;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          9 NAHLKQEIAALEQEIAALE 27
              |  ||:||| |: ||| |:
Db          1 NCMLKKEIAMLKLEIATLK 19


RESULT 12
US-10-076-622-587
; Sequence 587, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
;  APPLICANT: Houghton, Raymond L.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Persing, David H.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C11
;  CURRENT APPLICATION NUMBER: US/10/076,622
;  CURRENT FILING DATE:  2002-02-13
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 587
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-076-622-587

  Query Match             34.3%;  Score 47;  DB 14;  Length 21;
  Best Local Similarity   57.9%;  Pred. No. 20;
  Matches   11;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          9 NAHLKQEIAALEQEIAALE 27
              |  ||:||| |: ||| |:
Db          1 NCMLKKEIAMLKLEIATLK 19


RESULT 13
US-10-124-805-534
; Sequence 534, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:
;  APPLICANT: Houghton, Raymond L.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Persing, David H.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C12
;  CURRENT APPLICATION NUMBER: US/10/124,805
;  CURRENT FILING DATE:  2002-04-15
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 534
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-124-805-534

  Query Match             34.3%;  Score 47;  DB 14;  Length 21;
  Best Local Similarity   57.9%;  Pred. No. 20;
  Matches   11;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          9 NAHLKQEIAALEQEIAALE 27
              |  ||:||| |: ||| |:
Db          1 NCMLKKEIAMLKLEIATLK 19


RESULT 14
US-10-124-805-587
; Sequence 587, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:
;  APPLICANT: Houghton, Raymond L.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Persing, David H.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C12
;  CURRENT APPLICATION NUMBER: US/10/124,805
;  CURRENT FILING DATE:  2002-04-15
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 587
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-124-805-587
```

```
  Query Match            34.3%;  Score 47;  DB 14;  Length 21;
  Best Local Similarity  57.9%;  Pred. No. 20;
  Matches   11;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          9 NAHLKQEIAALEQEIAALE 27
              |  ||:||| |: ||| |:
Db          1 NCMLKKEIAMLKLEIATLK 19


RESULT 15
US-10-630-926-8
; Sequence 8, Application US/10630926
; Publication No. US20040194160A1
;   GENERAL INFORMATION:
;        APPLICANT: RICCARDI, Carlo
;        TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL
;                            DEATH PATHWAYS
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
;             STREET: 624 Ninth Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20001
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/630,926
;             FILING DATE: 31-Jul-2003
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/403,861A
;             FILING DATE: 11-Feb-2000
;             APPLICATION NUMBER: PCT/EP98/02490
;             FILING DATE: 27-APR-1998
;             APPLICATION NUMBER: EP 97107033.9
;             FILING DATE: 28-APR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: YUN, Allen C.
;             REGISTRATION NUMBER: 37,971
;             REFERENCE/DOCKET NUMBER: RICCARDI=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 26 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-630-926-8

  Query Match            32.8%;  Score 45;  DB 16;  Length 26;
  Best Local Similarity  42.9%;  Pred. No. 46;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KIRALKWKNAHLKQEIAALEQ 21
              |:  |  || ||: |:| |::
Db          4 KVEELLSKNYHLENEVARLKK 24


Search completed: April 27, 2005, 15:22:48
Job time : 90.5 secs
```

THIS PAGE LEFT BLANK